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96391

From: Kaushal, Sumesh
Sent: Wednesday, June 11, 2003 2:59 PM
To: STIC-Biotech/ChemLib
Subject: 09/663542: SEQ search

09/663542: SEQ search

Title: PHOSPHODIESTERASE ENZYMES
Inventor: FIDOCK, MARK

Please search

SEQ ID NO:1
SEQ ID NO:1 1-194

SEQ ID NO:2

priority : 01/21/00

thanks

S. Kaushal

CM1 12A07 AU1636

Ph: 703-305-6838

Mail Box: 11E12

CRFE

Searcher: _____
Phone: _____
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Date Picked Up: 6/13/03
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TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 2
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: 01/02
Sequence Sys.: 01/02
WWW/Internet: _____
Other (specify): _____

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File: 09663542

☒ IDS

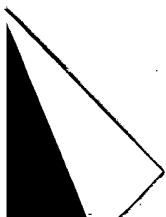
☒ SEQ Search -- Interference Search Removed ☒ 6/28/03

☒ Search Report -- In file []

[] Reference Cited

Notes:

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:46:07 ; Search time 5.52392 seconds
(without alignments)
1033.333 Million cell updates/sec

Title: US-09-663-542-1-copy_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNVLSTQWK.....VLLLEDIESPVVKFTKSFEL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307.5	31.5	875	1 US-08-480-547A-10	Sequence 10, Appl
2	307.5	31.5	875	1 US-08-480-547A-23	Sequence 23, Appl
3	307.5	31.5	875	1 US-08-250-847B-10	Sequence 10, Appl
4	307.5	31.5	875	1 US-08-250-847B-23	Sequence 23, Appl
5	307.5	31.5	875	2 US-08-463-949A-10	Sequence 10, Appl
6	307.5	31.5	875	2 US-08-463-949A-23	Sequence 23, Appl
7	307.5	31.5	875	3 US-08-464-410A-10	Sequence 10, Appl
8	307.5	31.5	875	3 US-08-464-410A-23	Sequence 23, Appl
9	307.5	31.5	875	3 US-09-226-741-5	Sequence 5, Appl
10	307.5	31.5	875	4 US-09-595-514-5	Sequence 5, Appl
11	307.5	31.5	875	5 PCT-US94-06066-23	Sequence 23, Appl
12	301.5	30.9	875	5 PCT-US94-06066-10	Sequence 10, Appl
13	186	19.1	367	4 US-09-226-741-3	Sequence 3, Appl
14	186	19.1	367	4 US-09-595-514-3	Sequence 3, Appl
15	186	19.1	490	3 US-09-226-741-1	Sequence 1, Appl
16	186	19.1	490	4 US-09-595-514-1	Sequence 1, Appl
17	165	16.9	766	2 US-09-951-648-2	Sequence 2, Appl
18	165	16.9	766	2 US-09-174-437-2	Sequence 2, Appl
19	165	16.9	779	2 US-08-951-648-6	Sequence 6, Appl
20	165	16.9	779	4 US-09-174-437-6	Sequence 6, Appl
21	165	16.9	803	2 US-08-951-648-4	Sequence 4, Appl
22	165	16.9	803	4 US-09-174-437-4	Sequence 4, Appl
23	162	16.6	905	4 US-09-754-250-4	Sequence 4, Appl
24	162	16.6	920	4 US-09-754-250-2	Sequence 2, Appl
25	162	16.6	941	1 US-07-872-644-45	Sequence 45, Appl
26	162	16.6	941	1 US-08-297-494-45	Sequence 45, Appl
27	162	16.6	941	1 US-08-297-510-45	Sequence 45, Appl

28	162	16.6	941	1 US-08-479-532-45	Sequence 45, Appl
29	162	16.6	941	1 US-08-455-526-45	Sequence 45, Appl
30	162	16.6	941	1 US-08-455-525-45	Sequence 45, Appl
31	162	16.6	941	3 US-09-139-491-45	Sequence 45, Appl
32	162	16.6	941	5 PCT-US92-03222-45	Sequence 45, Appl
33	154	15.8	921	1 US-07-872-644-39	Sequence 39, Appl
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35	154	15.8	921	1 US-08-297-510-39	Sequence 39, Appl
36	154	15.8	921	1 US-08-479-532-39	Sequence 39, Appl
37	154	15.8	921	1 US-08-455-526-39	Sequence 39, Appl
38	154	15.8	921	1 US-08-455-525-39	Sequence 39, Appl
39	154	15.8	921	3 US-09-139-491-39	Sequence 39, Appl
40	154	15.8	921	4 US-09-754-250-5	Sequence 5, Appl
41	154	15.8	921	5 PCT-US92-03222-39	Sequence 39, Appl
42	154	15.8	942	1 US-07-872-644-43	Sequence 43, Appl
43	154	15.8	942	1 US-08-297-494-43	Sequence 43, Appl
44	154	15.8	942	1 US-08-297-510-43	Sequence 43, Appl
45	154	15.8	942	1 US-08-479-532-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-480-547A-10
; Sequence 10, Application US/08480547A
; Patent No. 5652131
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlec, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,547A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5652131and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32791
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-547A-10

Query Match 31.5% Score 307.5; DB 1; Length 875;

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Db	367 CTIFIVDE 374

; Sequence 23, Application US/08463949A

APPLICANT: Ferguson, Kenneth M.
 APPLICANT: Francis, Sharron H.
 APPLICANT: Kadlecsek, Ann
 APPLICANT: Loughney, Kate
 APPLICANT: McAllister-Lucas, Linda M.
 APPLICANT: Sonnenburg, William K.
 APPLICANT: Thomas, Melissa K.
 TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
 TITLE OF INVENTION: Phosphodiesterase Materials and Methods
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,410A
 FILING DATE: June 5, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6037119and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/32705
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 875 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-464-410A-10

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RESULT 8
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; Sequence 23, Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecak, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Lind
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K

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RESULT 11
PCT-US94-06066-23
; Sequence 23, Application PC/TUS9406066
; GENERAL INFORMATION:
;
; APPLICANT: The Board of Regents of the University of Washington
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; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
;
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
;
; NUMBER OF SEQUENCES: 23
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;
; ADDRESSEE: Borun
;
; STREET: 6300 Sears Tower, 233 S. Wacker Drive

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; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,051
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-06066-23

Query Match 31.5%; Score 307.5; DB 5; Length 875;
Best Local Similarity 46.1%; Pred. No. 3.1e-26;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;

Qy 54 KDRFNDEIDKLTGYKTKSLCMLPIRSSDGIIGVQAQAIN-KIPEGAPFTTDEDEKVMQMY 112
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Qy 113 LPFGGIAISNAQLFAASRKEYERSALLEVVDNLFEEQTDLEKIVKIMHRAOTLLKCEER 172
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Db 367 CTIFIVDE 374

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; Sequence 10, Application PC/TUS9406066
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Washington
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06066
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,051
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-06066-10

Query Match 30.9%; Score 301.5; DB 5; Length 875;
Best Local Similarity 45.3%; Pred. No. 1.5e-25;
Matches 58; Conservative 32; Mismatches 37; Indels 1; Gaps 1;

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Qy 173 CSVLLLED 180
Db 357 CTIFIVDE 364

RESULT 13
US-09-226-741-3
; Sequence 3, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfeart, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: HSPDE10A2
; US-09-226-741-3

Query Match 19.1%; Score 186; DB 3; Length 367;
Best Local Similarity 29.7%; Pred. No. 6.1e-13;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;

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Qy 77 PIRSSDGEIIGVQAQAINKIPEGAPFTTDEDEKVMQMYLPFGGIAISNAQLFAASRKEYERS 136
Db 72 PIMNSHDIIGVQAQVNLRL-DGKPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQ 130
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77 PIRSSDGETIGVAQAINKIPEGAPTEDDDEKVMQMYLPFCGTAISNAQLFAASRKEYERS 136
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72 PIWNSNHQIIGVAQVLNRL-DGKPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKQ 130
137 RALLEVVN 144
131 SVALDVLS 138
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RESULT 14
US-09-595-514-3
; Sequence 3, Application US/09595514
; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDE10A2
US-09-595-514-3
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Query Match      19.1%; Score 186; DB 4; Length 367;
Best Local Similarity 29.7%; Pred. No. 6.1e-13;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;

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77 PIRSSDGETIGVAQAINKIPEGAPTEDDDEKVMQMYLPFCGTAISNAQLFAASRKEYERS 136
| | | | |
Db      72 PIWNSNHQIIGVAQVLNRL-DGKPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKQ 130
137 RALLEVVN 144
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RESULT 15
US-09-226-741-1
; Sequence 1, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDE10A1
US-09-226-741-1
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Query Match      19.1%; Score 186; DB 3; Length 490;
Best Local Similarity 29.7%; Pred. No. 9.3e-13;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;

QY      34 SLAEKOEK--HODFLIQRTKT-----KDRRFNDEIDKLTGYKTKSLLCM 76
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Result No.	Query			DB	ID	Description
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2	307.5	31.5	875	1	A48719	3',5'-cyclic-GMP p
3	205.5	21.1	862	2	I50186	3',5'-cyclic-GMP p
4	195	20.0	858	2	A34810	3',5'-cyclic-GMP p
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6	193	19.8	859	1	S06418	3',5'-cyclic-GMP p
7	189	19.4	859	2	B34611	3',5'-cyclic-GMP p
8	186	19.1	856	1	A47451	3',5'-cyclic-GMP p
9	183	18.8	854	2	A42828	3',5'-cyclic-GMP p
10	183	18.8	859	2	S13030	3',5'-cyclic-GMP p
11	180.5	18.5	393	2	T25590	hypothetical prote
12	180	18.5	800	2	S13032	3',5'-cyclic-GMP p
13	180	18.5	856	2	S30762	3',5'-cyclic-GMP p
14	178.5	18.3	860	2	AB2044	adenylate cyclase
15	174.5	17.9	859	2	AC2089	adenylate cyclase
16	170	17.4	853	2	A36617	3',5'-cyclic-GMP p
17	159	16.3	928	1	JC2486	3',5'-cyclic-nucle
18	154	15.8	921	1	A40981	3',5'-cyclic-nucle
19	129	13.2	944	2	AC2073	two-component sens
20	118.5	12.2	1245	2	D71613	GAF domain protein
21	118.5	12.2	1850	2	AC1917	serine/threonine k
22	116	11.9	1900	2	AG2391	serine/threonine k
23	111.5	11.4	573	2	B70942	hypothetical prote
24	100	10.3	841	1	S24462	probable 3',5'-cyc
25	100	10.3	918	2	D88544	protein R08D7.6 [i
26	95	9.7	1808	2	AB1847	serine/threonine k
27	94.5	9.7	578	2	E70645	hypothetical prote
28	94	9.6	1777	2	AC2088	serine/threonine k
29	92.5	9.5	1449	2	G81419	hypothetical prote

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Qy      118  IATSNALQFAASRKKEYRSRALLEVNDLFEETQDTLEKIVYKIMHRAQTLLKGCERSVLL 277
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Qy      178  LE 179
          |
Db      278  LD 279

RESULT 10
S13030
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S13030
R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A/Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase of the beta-subunit gene.
A/Reference number: S13030; PMID:91130581; PMID:1847109

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<hr/>					
A; Residues:	1-839	<BAE>			
C; Cross-references:	EMBL:X60664;	NID:g53587;	PIDN:CAA43072.1;	PID:g53588	
C; Superfamily:	3',5'-cyclic-GMP phosphodiesterase alpha chain;	3',5'-cyclic-nuc.			
C; Keywords:	COMP binding; phosphoric diester hydrolase				
F; 558-791/Domain:	3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>				
<hr/>					
Query Match	18.8%	Score 183;	DB 2;	Length 859;	
Best Local Similarity	34.1%;	Pred. No. 4.5e-07;			
Matches	43;	Conservative 27;	Mismatches 54;	Indels 2;	Gaps 2;
<hr/>					
Qy	54	KDRFRDEIDKLTGYKTSLCLLCPIRSSDGEILGVAQAINKIPEGAPFTTDDKEVQMOMYL	113		
Dd	158	EDGHCFDVNLFEYQTKNLSPIMNGK-DVVAIIMAVNKIDE-PHETKRDEEILLKYL	215		
<hr/>					
Qy	114	PFGCIAISNAQLFAASRKEYERSALLFVNVDLFEEQTDLKTVKKIMIRAOPLLLKCERC	173		
Dd	216	NFYNLIMKYFHLSYLNCETRRGOILLWSGSKFEEELTDIEROFKALYTVTRAFNLCDRY	275		
<hr/>					
Qy	174	SVLLE	179		
Dd	276	SVGLLD	281		

A;Description: The sequence of C. elegans cosmid C3E12.
A;Reference number: Z20055
A;Accession: T25590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-393 <WIL>
A;Cross-references: EMBL:080032; PIDN:AA853879.1; GSPDB:GN00019; CESP:C32E12.2
A;Experimental source: strain Bristol N2; clone C32E12
C;Genetics:
A;Gene: CESP:C32E12.2
A;Map position: 1
A;Introns: 52/2; 137/2; 166/2; 217/3; 327/2
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
F;189-393/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NCD>

A: Introns: 32/72; 131/21; 166/23; 211/33; 321/12
 C: Superfamily: 3', 5'-cyclic-nucleotide phosphodiesterase homology
 F: 189-393/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>
 Query Match 18.5%; Score 180.5; DB 2; Length 393;
 Best Local Similarity 40.0%; Pred. No. 2.9e-07;
 Matches 36; Conservative 20; Mismatches 31; Indels 3; Gaps 2;
 QY 54 KDRFRNDEIKDTGYTKTSILLCPIRSSDGEIIGVAQAINKIPEGAFTTDEDEKVMQMYL 113

[illegible]

Search completed: June 13, 2003, 15:49:43
Job time : 8.51253 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:49 ; Search time 3.97722 Seconds
(without alignments)
2023.123 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNLSATQWK.....VLLLEDIESPVVVKFSFEL 194

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	308.5	31.6	833	1 CN5A.RAT	O54735 rattus norv
2	307.5	31.5	865	1 CN5A.BOVIN	Q28156 bos taurus
3	307.5	31.5	865	1 CN5A.CANFA	O77746 canis faml
4	307.5	31.5	875	1 CN5A.HUMAN	O76074 homo sapien
5	205.5	21.1	862	1 CNRC.CHICK	P52731 gallus gall
6	195	20.0	855	1 CNRC.BOVIN	P16586 bos taurus
7	191	19.6	858	1 CNRC.HUMAN	P51160 homo sapien
8	189	19.4	858	1 CNRA.BOVIN	P11541 bos taurus
9	189	19.4	859	1 CNRA.HUMAN	P18499 homo sapien
10	183	18.8	854	1 CNRB.HUMAN	P35913 homo sapien
11	183	18.8	856	1 CNRB.CANFA	P33726 canis faml
12	183	18.8	858	1 CNRA.MOUSE	P27664 mus musculus
13	183	18.8	860	1 CNRA.CANFA	Q28263 canis faml
14	180.5	18.5	393	1 YB2J.CAEEL	P91119 caenorhabdi
15	175	17.9	856	1 CNRB.MOUSE	P23440 mus musculus
16	170	17.4	853	1 CNRB.BOVIN	P23439 bos taurus
17	165	16.9	779	1 CN10.HUMAN	Q9Y233 homo sapien
18	162	16.6	941	1 CN2A.HUMAN	Q00408 homo sapien
19	159	16.3	928	1 CN2A.RAT	Q01062 rattus norv
20	154	15.8	921	1 CN2A.BOVIN	P14099 bos taurus
21	100	10.3	918	1 YNE6.CAEEL	P30645 caenorhabdi
22	86.5	8.9	1855	1 MY5A.HUMAN	Q9Y411 homo sapien
23	86	8.8	496	1 IMDH.METJA	Q59011 methanococc
24	85.5	8.8	821	1 LIN5.CAEEL	P45970 caenorhabdi
25	84.5	8.7	1828	1 MY5A.RAT	Q9QVf3 rattus norv
26	84	8.6	2869	1 RBP1.PLAVB	Q00798 plasmodium
27	82.5	8.5	1853	1 MY5A.MOUSE	Q99104 mus musculus
28	82	8.4	859	1 MUTS.AQUAE	O66652 aquifex aeo
29	81.5	8.4	3726	1 TRX.DROME	P20659 drosophila
30	81	8.3	2153	1 POLG.HRV16	Q82122 human rhino
31	80.5	8.3	3421	1 TEGU.HSVER	P28955 equine herp
32	79.5	8.2	171	1 YF87.METJA	Q58982 methanococc
33	79	8.1	220	1 Y231.RICPR	Q92du3 rickettsia

RESULT 1

ID	CNSA_RAT	STANDARD;	PRT;	833 AA.
AC	O54735;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)			
DE	(CGMP-binding CGMP-specific phosphodiesterase).			
GN	PDE5A OR PDE5.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; TISSUE=Lung;			
RX	MEDLINE=98036118; PubMed=9370351;			
RA	Kotera J., Yanaka N., Fujishige K., Imai Y., Akatsuka H., Ishizuka T.,			
RA	Kawashima K., Omori K.;			
RT	"Expression of rat CGMP-binding CGMP-specific phosphodiesterase mRNA			
RT	in Purkinje cell layers during postnatal neuronal development.";			
RL	Eur. J. Biochem. 249:434-442(1997).			
CC	FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE			
CC	INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS			
CC	PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-			
CC	GMP.			
CC	FUNCTION: CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =			
CC	guanosine 5'-phosphate.			
CC	COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR			
CC	CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).			
CC	PATHWAY: Cyclic nucleotide metabolism.			
CC	ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 AND PDE5A2 (SHOWN HERE);			
CC	ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO			
CC	POTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN			
CC	WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A			
CC	AND B.			
CC	PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO			
CC	ALLOSTERIC SITES (BY SIMILARITY).			
CC	SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE			
CC	FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: D89093; BAA23672.1;			
DR	InterPro: IPR003018; GAF.			
DR	InterPro: IPR003607; ME_Plpase_HDC.			
DR	InterPro: IPR002073; PDEase.			

ALIGNMENTS

34	78.5	8.1	263	1	ISTB_BACFR	Q45120 bacteroides
35	78.5	8.1	509	1	RA18_MOUSE	Q9gxk2 mus musculus
36	78.5	8.1	863	1	IMB1_SCHPO	O13864 schizosacch
37	78.5	8.1	882	1	RA50_PYRFU	P58301 pyrococcus
38	78.5	8.1	1972	1	MYHB_RABIT	P35748 oryctolagus
39	78	8.0	458	1	DESM_XENLA	P23239 xenopus lae
40	78	8.0	648	1	GRT1_SCHPO	Q9c469 schizosacch
41	78	8.0	880	1	RA50_PYRAB	Q9uzc8 pyrococcus
42	77.5	7.9	810	1	Y555_HUMAN	Q96aa8 homo sapien
43	77.5	7.9	1225	1	SMC1_YEAST	P32908 saccharomyc
44	77	7.9	566	1	UVRP_AQUAE	O67887 aquifex aeo
45	77	7.9	722	1	YC06_KLEPN	Q48452 klebsiella

DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CGMP; CGMP-binding; Phosphorylation; Alternative splicing;
Zinc; Repeat.
FT NP_BIND 196 279 CGMP (BY SIMILARITY).
FT NP_BIND 378 468 CGMP (BY SIMILARITY).
FT BINDING 244 244 CGMP (BY SIMILARITY).
FT BINDING 245 245 CGMP (BY SIMILARITY).
FT BINDING 257 257 CGMP (BY SIMILARITY).
FT BINDING 446 446 CGMP (BY SIMILARITY).
FT DOMAIN 546 811 CATALYTIC (BY SIMILARITY).
FT MOD_RES 60 60 PHOSPHORYLATION (POTENTIAL).
FT METAL 571 571 ZINC 1 (POTENTIAL).
FT METAL 575 575 ZINC 1 (POTENTIAL).
FT METAL 600 600 ZINC 1 (POTENTIAL).
FT METAL 611 611 ZINC 2 (POTENTIAL).
FT METAL 615 615 ZINC 2 (POTENTIAL).
FT METAL 640 640 ZINC 2 (POTENTIAL).
SQ SEQUENCE 833 AA; 94556 MW; 712DC159C80CB09D CRC64;
Query Match 31.6%; Score 308.5; DB 1; Length 833;
Best Local Similarity 43.7%; Pred. No. 1.7e-18;
Matches 62; Conservative 34; Mismatches 43; Indels 3; Gaps 2;
QY 54 KDRRENDEIDKLTGYKTKSLCLMPTRSSDGEIIGVQAQAIN-KIPGAPFTEDDEKVMQMY 112
DB 205 EDPRNEAEVDQITGYKTSILCMPIKNHREEVGVQAQINKSGNGGTFTEKDEKDEFAAY 264
QY 113 LPFGCIATISNAQLPAASKEYERSRALLVNDLPFEOTDLEKIVKTKMHAQTLLKCKER 172
DB 265 LAFGCIIVHNAQLYTSILEKRNQVLLDLASLIFEQOQSLEVLTKKTAANTIIISMVQVK 324
QY 173 CSVLLEDIESPVVFKTSFEL 194
DB 325 CTIFIVD--EDCPDSFSRVQM 344

RESULT 2

CNSA_BOVIN
ID CNSA_BOVIN STANDARD; PRT: 865 AA.
AC Q28156;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
DE (CGMP-binding CGMP-specific phosphodiesterase).
GN PDE5A OR PDE5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=94043054; PubMed=8226796;
RA McAllister-Lucas L.M., Sonnenburg W.K., Kadlecsek A., Seger D.,
RA Trong H.L., Colbran J.L., Thomas M.K., Walsh K.A., Francis S.H.,
RA Corbin J.D., Beavo J.A.;
RT "The structure of a bovine lung CGMP-binding, CGMP-specific
phosphodiesterase deduced from a cDNA clone.";
RL J. Biol. Chem. 268:22863-22873(1993).
RN [2]
RP METAL-BINDING.
RX MEDLINE=94357882; PubMed=8077192;
RA Francis S.H., Colbran J.L., McAllister-Lucas L.M., Corbin J.D.;
RT "Zinc interactions and conserved motifs of the CGMP-binding CGMP-
specific phosphodiesterase suggest that it is a zinc hydrolase.";
RL J. Biol. Chem. 269:22477-22480(1994).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=96107229; PubMed=8530505;
RA McAllister-Lucas L.M., Haik T.L., Colbran J.L., Sonnenburg W.K.,
RA Seger D., Turko I.V., Beavo J.A., Francis S.H., Corbin J.D.;
RT "An essential aspartic acid at each of two allosteric CGMP-binding
sites of a CGMP-specific phosphodiesterase.";
RL J. Biol. Chem. 270:30671-30679(1995).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=96355629; PubMed=8703039;
RA Turko I.V., Haik T.L., McAllister-Lucas L.M., Burns F., Francis S.H.,
RA Francis S.H., Corbin J.D.;
RT "Identification of key amino acids in a conserved CGMP-binding site of
CGMP-binding phosphodiesterases. A putative NKxnd motif for CGMP
binding.";
RL J. Biol. Chem. 271:22240-22244(1996).
RN [5]
RP PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=98109724; PubMed=9445376;
RA Turko I.V., Francis S.H., Corbin J.D.;
RT "Binding of CGMP to both allosteric sites of CGMP-binding CGMP-
specific phosphodiesterase (PDE5) is required for its
phosphorylation.";
RL Biochem. J. 329:505-510(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS.
CC -!- ENZYME REGULATION: MOST POTENTLY INHIBITED BY ZAPRINAST AND
DIPYRIDAMOLE.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
ALLOSTERIC SITES.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
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EMBL; L16545; AAB00990.1; -
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CGMP; CGMP-binding; Phosphorylation; Zinc; Repeat.
FT MOD_RES 92 92 PHOSPHORYLATION (POTENTIAL).
FT METAL 603 603 ZINC 1 (POTENTIAL).
FT METAL 607 607 ZINC 1 (POTENTIAL).
FT METAL 632 632 ZINC 1 (POTENTIAL).
FT METAL 643 643 ZINC 2 (POTENTIAL).
FT METAL 647 647 ZINC 2 (POTENTIAL).
FT METAL 672 672 ZINC 2 (POTENTIAL).
FT NP_BIND 228 311 CGMP.

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FT NP_BIND 410 500 CGMP.
FT BINDING 276 276 CGMP.
FT BINDING 277 277 CGMP.
FT BINDING 289 289 CGMP.
FT BINDING 478 478 CGMP.
FT DOMAIN 578 843 CATALYTIC (BY SIMILARITY).
FT MUTAGEN 276 276 N->A: DECREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 277 277 K->A: DECREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 277 277 K->R: SLIGHT INCREASE IN CGMP-BINDING.
FT MUTAGEN 289 289 D->A: DECREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 289 289 D->N: INCREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY.
FT MUTAGEN 290 290 E->A: NO CHANGE IN CGMP-BINDING.
FT MUTAGEN 478 478 D->A: INCREASED CGMP-BINDING; NO CHANGE
IN CATALYTIC ACTIVITY. PHOSPHORYLATED AT
LOWER CONCENTRATIONS OF CGMP.
SQ SEQUENCE 865 AA; 98626 MW; 2FF7144B2990B4F7 CRC64;

Query Match 31.5%; Score 307.5; DB 1; Length 865;
Best Local Similarity 46.1%; Pred. No. 2.2e-18;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;

QY 54 KDRFNDEIDKLTGYKTSLLCMPIRSSDGEIIGVQAQAIN-KIPEGAPFTDEDEKVMQMY 112
DB 237 EDPRFNAEVDQITGYKTQSILCMPKNHREEVGVQAQINKSGNGGFTTEKDEKDFAA 296

QY 113 LPFGGIALSNAQLFAASRKEYERSALLLEVNDLFEEQTDLEKIVKIMHRAOTLLKCE 172
DB 297 LAFCGVLHNAQLYETSLLENKRNQVLLDLASLIFEQQSLEVLKTKAATIIISFMQVOK 356

QY 173 CSVLLED 180
DB 357 CTIFIVDE 364

RESULT 3
ID CNSA_CANFA STANDARD; PRT; 865 AA.
AC 077746; 077747;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
DE (CGMP-binding CGMP-specific phosphodiesterase).
GN PDE5A OR PDE5.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS PDE5A1 AND PDE5A2).
RC TISSUE=Lung;
RX MEDLINE=98434620; PubMed=9756948;
RA Kotera J., Fujishige K., Akatsuka H., Inai Y., Yanaka N., Omori K.;
RT "Novel alternative splice variants of CGMP-binding CGMP-specific
phosphodiesterase."
RL J. Biol. Chem. 273:26982-26990(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2O) =
guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY ZAPRINAST.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- SUBCELLULAR LOCATION: PDE5A1 AND PDE5A2 ARE LOCATED MOSTLY TO
SOLUBLE CELLULAR FRACTIONS AND SOME TO PARTICULATE CELLULAR
FRACTIONS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 (SHOWN HERE) AND PDE5A2;
ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: BOTH ISOFORMS EXPRESSED ABUNDANTLY IN THE
CEREBELLUM, HIPPOCAMPUS, RETINA, LUNG, HEART, SPLEEN AND THORACIC
ARTERY. PDE5A1, BUT NOT PDE5A2, IS ALSO ABUNDANTLY EXPRESSED IN
THE PYLORUS.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
ALLOSTERIC SITES (BY SIMILARITY).
CC -!- MISCELLANEOUS: CGMP-BINDING TO THE ALLOSTERIC SITES IS STIMULATED
BY 3-ISOBUTYL-1-METHYLXANTHINE (IBMX).
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY.
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EMBL; AB008467; BAA33503.1; -
EMBL; AB008468; BAA33504.1; -
InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDC.
InterPro; IPR002073; PDEase.
Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
PRINTS; PR00387; PDJESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CGMP; CGMP-binding; Phosphorylation; Alternative splicing;
Zinc; Repeat.
KW NP_BIND 228 311 CGMP (BY SIMILARITY).
FT NP_BIND 410 500 CGMP (BY SIMILARITY).
FT BINDING 276 276 CGMP (BY SIMILARITY).
FT BINDING 277 277 CGMP (BY SIMILARITY).
FT BINDING 289 289 CGMP (BY SIMILARITY).
FT BINDING 478 478 CGMP (BY SIMILARITY).
FT DOMAIN 578 843 CATALYTIC (BY SIMILARITY).
FT MOD_RES 92 92 PHOSPHORYLATION (POTENTIAL).
FT METAL 603 603 ZINC 1 (POTENTIAL).
FT METAL 607 607 ZINC 1 (POTENTIAL).
FT METAL 632 632 ZINC 1 (POTENTIAL).
FT METAL 643 643 ZINC 2 (POTENTIAL).
FT METAL 647 647 ZINC 2 (POTENTIAL).
FT METAL 672 672 ZINC 2 (POTENTIAL).
FT VARSPPLIC 1 40 MERGSPGAGAAALPRDQDSVEAWLDDHDDHDDFTSFYVKKAT
FT -> MLFPGHQR (IN ISOFORM PDE5A2).
SQ SEQUENCE 865 AA; 98293 MW; F20BB37B71E93BB6 CRC64;

Query Match 31.5%; Score 307.5; DB 1; Length 865;
Best Local Similarity 46.1%; Pred. No. 2.2e-18;
Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;

QY 54 KDRFNDEIDKLTGYKTSLLCMPIRSSDGEIIGVQAQAIN-KIPEGAPFTDEDEKVMQMY 112
DB 237 EDPRFNAEVDQITGYKTQSILCMPKNHREEVGVQAQINKSGNGGFTTEKDEKDFAA 296

QY 113 LPFGGIALSNAQLFAASRKEYERSALLLEVNDLFEEQTDLEKIVKIMHRAOTLLKCE 172
DB 297 LAFCGVLHNAQLYETSLLENKRNQVLLDLASLIFEQQSLEVLKTKAATIIISFMQVOK 356

QY 173 CSVLLED 180
DB 357 CTIFIVDE 364
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QY 54 KDRRENDEIKLTGYKTKSLCMLPIRSRSDGEIIGVQAQIN-KIPGAPFTEDEKVMQY 112
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 EDPREAEVDQITGYKTKSLCMLPIKHNREEVGVQAQINKSGNGTTEKDEKDFRAY 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 LPFGCIATSNALQFAASKEYERSRALLLEVNDLFEEQTDLEKIVKIMHRAQTLLKCE 172
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 LAFCVILHNAQLYETSLLENKRNOVLDSLAFIEQOQSLEVLKIAATIISPMQVOK 366
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 173 CSVLLED 180
:|||||:
Db 367 CTIFIVDE 374

RESULT 5
CNRC_CHICK STANDARD; PRT; 862 AA.
ID CNRC_CHICK
AC P52731;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
DE (EC 3.1.4.17).
GN PDE6C.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rhode Island red; TISSUE=Retina;
RX MEDLINE=95121406; PubMed=7821382;
RA Sample=Rowland S.L., Green D.A.;
RA "Molecular characterization of the alpha'-subunit of cone
RT photoreceptor cGMP phosphodiesterase in normal and rd chicken.";
RL Exp. Eye Res. 59:365-372(1994).
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED
CC WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 KDa.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC
CC EMBL; L29233; AAC4223.1; -
CC InterPro; IPR003018; GAF.
CC InterPro; IPR003607; ME.Pplase_Hdc.
CC InterPro; IPR002073; PDEase.
CC InterPro; IPR001230; Prenyl_site.
CC Pfam; PF00233; PDEase; 1.
CC Pfam; PF01590; GAF; 2.
CC PRINTS; SM00065; GAF; 2.
CC SMART; SM00471; Hdc; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
FT LIPID 859 859 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 862 AA; 100008 MW; B03145B5F5F26A8 CRC64;

Query Match 21.1%; Score 205.5; DB 1; Length 862;
Best Local Similarity 29.4%; Pred. No. 8.5e-10;
Matches 53; Conservative 34; Mismatches 60; Indels 33; Gaps 4;
QY 25 TRLVQISGASLAEQKQKHODFLIQRTKT-----KDRRFN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
Db 112 TRLLNVTPS-----KFEDNLVNDPKETVPFLDIGIAGVVAHTKKFFNIPDVKKNNHFS 165
QY 60 DEIDKLTGYKTKSLCMLPIRSRSDGEIIGVQAQIN-KIPGAPFTEDEKVMQYLPFCGIA 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166 DYLDKKTGTGTTVMMAIPI-TQGEVLAVVWALNAL-NASEFSKDEDEVKKYLNFISLV 223
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 ISNAOLFASRKEYERSRALLLEVNDLFEEQTDLEKIVKIMHRAQTLLKCEKRCVLLLE 179
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 224 LRNHHTSYLYNIESRSQMLLSANKVFEELTDIERQHFHAKYLTIRMYLNCERYSVGLLD 283

RESULT 6
CNRC_BOVIN STANDARD; PRT; 855 AA.
ID CNRC_BOVIN
AC P16586;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
DE (EC 3.1.4.17) (PDE V-C1).
GN PDE6C OR PDEA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90115860; PubMed=2153291;
RX Li T., Volpp K., Applebury M.L.;
RT "Bovine cone photoreceptor cGMP phosphodiesterase structure deduced
RL from a cDNA clone.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:293-297(1990).
RN [2]
RP SEQUENCE OF 308-502 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=90115859; PubMed=2153290;
RX Charbonneau H., Prusti R.K., Letrong H., Sonnenburg W.K.,
RA Mullaney P.J., Walsh K., Beavo J.A.;
RA "Identification of a noncatalytic cGMP-binding domain conserved in
RT both the cGMP-stimulated and photoreceptor cyclic nucleotide
RT phosphodiesterases.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:288-292(1990).
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED
CC WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 KDa.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC
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CC
CC EMBL; M37838; AAA30687.1; -
CC EMBL; M33140; AAA30688.1; -
CC PIR; A34810; A34810.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR003607; ME.Pplase_Hdc.
CC InterPro; IPR002073; PDEase.
CC InterPro; IPR001230; Prenyl_site.
CC Pfam; PF00233; PDEase; 1.
CC Pfam; PF01590; GAF; 2.
CC PRINTS; SM00387; PDIESTERASE1.
CC SMART; SM00065; GAF; 2.
CC SMART; SM00471; Hdc; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
FT LIPID 852 852 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 855 AA; 98797 MW; 1FCFFD045686D65 CRC64;
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Query Match      20.0%; Score 195; DB 1; Length 855;
Best Local Similarity 36.5%; Pred. No. 6.5e-09;
Matches 46; Conservative 25; Mismatches 53; Indels 2; Gaps 2;

QY 54 KDRFNDEIDKLTGYTKSLCMPTRSSDGETIIGVAAQAINKEPAGPTEDEKVMQMYL 113
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 155 KNSHSDPMDKOTGYVTRNLLATPVMGK-EVLAVFMAVNV-NASEFSKQDEEVFSKYL 212
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:

QY 114 PFCGTAISNAQLFAASRKEYESRALLEVNDLFEEOTDLEKIVKIMHRAQTLLKCERC 173
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 213 SEVSIILKHTNYLYNIESRSQILMWSANKVFEELTDVERQPHKALYTVRSLNCERY 272

QY 174 SVLLE 179
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 273 SIGLLD 278

RESULT 7
CNRC_HUMAN
ID CNRC_HUMAN STANDARD; PRT; 858 AA.
AC P51160;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cone cGMP-specific 3',5'-cyclic phosphodiesterase alpha'-subunit
DE (EC 3.1.4.17).
GN PDE6C OR PDEA2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96039253; PubMed=7490077;
RA Piriev N.I., Viczian A.S., Ye J., Kerner B., Korenberg J.R.,
RA Farber D.B.;
RT "Gene structure and amino acid sequence of the human cone
RT photoreceptor cGMP-phosphodiesterase alpha' subunit (PDEA2) and its
RT chromosomal localization to 10q24."
RL Genomics 28:429-435(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Piriev N.I., Viczian A., Ye J., Farber D.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Feshchenko E.A.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2O) -
CC -!- guanosine 5'-phosphate.
CC -!- SUBUNIT: COMPOSED OF TWO ALPHA' SUBUNITS THAT ARE ASSOCIATED
CC WITH 3 SMALLER PROTEINS OF 11, 13, AND 15 KDa.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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DR EMBL; U20212; AAA92886.1; JOINED.
DR EMBL; U20217; AAA92886.1; JOINED.
DR EMBL; U20196; AAA92886.1; JOINED.
DR EMBL; U20197; AAA92886.1; JOINED.
DR EMBL; U20199; AAA92886.1; JOINED.
DR EMBL; U20200; AAA92886.1; JOINED.
DR EMBL; U20201; AAA92886.1; JOINED.
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DR EMBL; U20202; AAA92886.1; JOINED.
DR EMBL; U20203; AAA92886.1; JOINED.
DR EMBL; U20204; AAA92886.1; JOINED.
DR EMBL; U20205; AAA92886.1; JOINED.
DR EMBL; U20206; AAA92886.1; JOINED.
DR EMBL; U20207; AAA92886.1; JOINED.
DR EMBL; U20208; AAA92886.1; JOINED.
DR EMBL; U20209; AAA92886.1; JOINED.
DR EMBL; U20210; AAA92886.1; JOINED.
DR EMBL; U20211; AAA92886.1; JOINED.
DR EMBL; X94354; CAA64079.1;
DR MIM; 600827;
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Ppase_HDC.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane.
FT LIPID 855 855
FT CONFLICT 116 116 V -> D (IN REF. 3).
FT CONFLICT 270 270 S -> T (IN REF. 3).
FT CONFLICT 373 373 Q -> P (IN REF. 1).
FT CONFLICT 464 464 P -> L (IN REF. 1).
FT CONFLICT 565 565 Q -> R (IN REF. 3).
SQ SEQUENCE 858 AA; 99102 MW; 3D1535C21780A56E CRC64;

Query Match      19.6%; Score 191; DB 1; Length 858;
Best Local Similarity 36.5%; Pred. No. 1.4e-08;
Matches 46; Conservative 24; Mismatches 54; Indels 2; Gaps 2;

QY 54 KDRFNDEIDKLTGYTKSLCMPTRSSDGETIIGVAAQAINKEPAGPTEDEKVMQMYL 113
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 160 KNSHSDPMDKOTGYVTRNLLATPVMGK-EVLAVFMAVNV-NASEFSKQDEEVFSKYL 217
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:

QY 114 PFCGTAISNAQLFAASRKEYESRALLEVNDLFEEOTDLEKIVKIMHRAQTLLKCERC 173
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 218 NFVSIILRLHTSYMYNIESRSQILMWSANKVFEELTDVERQPHKALYTVRSLNCERY 277

QY 174 SVLLE 179
   I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I: I:
Db 278 SIGLLD 283
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RESULT 8

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CNRA_BOVIN
ID CNRA_BOVIN STANDARD; PRT; 858 AA.
AC P11541;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
DE (EC 3.1.4.17) (GMP-PDE alpha) (PDE V-B1).
GN PDE6A OR PDEA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169986; PubMed=2155175;
RX Pittler S.J., Baehr W., Wasmuth J.J., McConnell D.G., Champagne M.S.,
RA Vautanen P., Ledbetter D., Davis R.L.;
RT "Molecular characterization of human and bovine rod photoreceptor
RT cGMP phosphodiesterase alpha-subunit and chromosomal localization of
RL the human gene."
RL Genomics 6:272-283(1990).
```

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RN      [2]
RC      SEQUENCE FROM N.A.
RC      TISSUE=Retina;
RX      MEDLINE=88082056; PubMed=2826095;
RA      Yu A., Ovchinnikov A., Gubanov V.V., Khrantsov N.V.,
RA      Akhmedov N.B., Ischenko K.A., Zagranichnyi V.E.,
RA      Vasilevskaya I.A., Rakitina T.V., Atabekova N.V., Barinov A.A.,
RA      Muradov K.G., Shuvaeva T.M., Byistrov N.S., Severtsova I.V.,
RA      Lipkin V.M.;
RT      "Cyclic GMP phosphodiesterase from the bovine retina. Amino acid
RT      sequence of the alpha-subunit and nucleotide sequence of corresponding
RT      cDNA."
RL      Dokl. Akad. Nauk SSSR 296:487-491(1987).
RN      [3]
RC      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX      MEDLINE=88030033; PubMed=2822478;
RA      Ovchinnikov Y.A., Gubanov V.V., Khrantsov N.V., Ischenko K.A.,
RA      Zagranichnyi V.E., Muradov K.G., Shuvaeva T.M., Lipkin V.M.;
RT      "Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence
RT      of the alpha-subunit and nucleotide sequence of the corresponding
RT      cDNA."
RL      FEBS Lett. 223:169-173(1987).
CC      -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC      TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC      -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC      guanosine 5'-phosphate.
CC      -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC      BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC      -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC      FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X12756; CAA31243.1; -
DR      EMBL; M27541; AAA30441.1; -
DR      EMBL; M36683; AAA30442.1; -
DR      EMBL; M26043; AAA30443.1; -
DR      PIR; S06418; S06418.
DR      PIR; A34611; A34611.
DR      InterPro; IPR003018; GAF.
DR      InterPro; IPR0033607; MEPlase_Hdc.
DR      InterPro; IPR002073; PDEase.
DR      InterPro; IPR001230; Prenyl_site.
DR      Pfam; PF00233; PDEase; 1.
DR      Pfam; PF01590; GAF; 2.
DR      PRINTS; PR00387; PD1ESTERASE1.
DR      SMART; SM00065; GAF; 2.
DR      SMART; SM00471; Hdc; 1.
DR      PROSITE; PS00126; PDEASE_I; 1.
KW      Hydrolase; CGMP; Vision; Prenylation; Lipoprotein; Acetylation.
FT      INIT_MET 0
FT      MOD_RES 1
FT      LIPID 855 855
FT      VARIANT 380 380
FT      CONFLICT 193 193
FT      CONFLICT 423 423
FT      CONFLICT 674 674
FT      CONFLICT 858 AA; 99209 MW; 86624E43662A95CC CRC64;
SQ      SEQUENCE 858 AA; 99209 MW; 86624E43662A95CC CRC64;

Query Match 19.4%; Score 189; DB 1; Length 858;
Best Local Similarity 33.3%; Pred. No. 2.1e-08;
Matches 42; Conservative 29; Mismatches 53; Indels 2; Gaps 2;

OY      54 KDRFRNDEIKLTGYTKTSLCMLPIRSSDGEIIGVQAQAINKIPGAPFTEDDEKVMQMYL 113
DB      157 EDEHCFDFTDYTEYTKNLIASPMNGK-DVVAILVMVKNV-DGPHFTEENDEILKYL 214

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QY      114 PFGGIAISNAQLFAASRKEYERSRALLEVNVNDFEEQTDLKIVKKHRAOTLLKCERC 173
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      215 NFANLIMKVPHLSYLHCNCETRRGQILLWSGSKVFEELTDIERGHKALYTVPRAFNCDRY 274
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      174 SVLLLE 179
       |||||
Db      275 SVGLLD 280

RESULT 9
CNRA_HUMAN          STANDARD;      PRF;    859 AA.
ID ID CNRA_HUMAN
AC P16499;
DT DT 01-AUG-1990 (Rel. 15, Created)
DT DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
GN GN (EC 3.1.4.17) (CMP-PDE alpha) (PDE V-B1).
DN DN PDE6A OR PDEA.
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX OX NCBI_TaxID=9606;
RN RN [1]
RX RX SEQUENCE FROM N.A.
RA RA MEDLINE=90169986; PubMed=2151175;
RA RA Pittler S.J., Baehr W., Dryja T.P., Wasmuth J.J., McConnell D.G.,
RT RT Champagne M.S., Grondin V., Vantuinen P., Ledbetter D., Davis R.L.;
RT RT "Molecular characterization of human and bovine rod photoreceptor
RT RT cGMP phosphodiesterase alpha-subunit and chromosomal localization of
RT RT the human gene.";
RL RL Genomics 6:272-283(1990).
RN RN [2]
RP RP REVISION TO 845-848.
RA RA Pittler S.J., Baehr W., Wasmuth J.J., McConnell D.G.,
RA RA Champagne M.S., Vantuinen P., Ledbetter D., Davis R.L.;
RL RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN RN [3]
RP RP VARIANT ARRP ARG-343.
RX RX MEDLINE=96083603; PubMed=7493036;
RA RA Huang S.H., Pittler S.J., Huang X., Oliveira L., Berson E.L.,
RA RA Dryja T.P.;
RT RT "Autosomal recessive retinitis pigmentosa caused by mutations in the
RT RT alpha subunit of rod cGMP phosphodiesterase.";
RL RL Nat. Genet. 11:468-471(1995).
CC CC -1- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF TRANSMISSION
CC CC AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC CC -1- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC CC guanosine 5'-phosphate.
CC CC -1- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC CC -1- DISEASE: DEFECTS IN PDE6 ARE A CAUSE OF AUTOSOMAL DOMINANT
CC CC RETINITIS PIGMENTOSA (ADRP) OR AUTOSOMAL RECESSIVE RP (ARRP).
CC CC PATIENTS TYPICALLY HAVE NIGHT VISION BLINDNESS AND LOSS OF
CC CC MIDPERIPHERAL VISUAL FIELD; AS THEIR CONDITION PROGRESSES, THEY
CC CC LOOSE THEIR FAR PERIPHERAL VISUAL FIELD AND EVENTUALLY CENTRAL
CC CC VISION AS WELL.
CC CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC CC FAMILY.
CC CC -1- DATABASE: NAME=Mutations of the PDE6A/B/G genes;
CC CC NOTE=Retina International's Scientific Newsletter;
CC CC WWW="http://www.retina-international.com/sci-news/pdemut.htm".
-----
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or send an email to license@isb-sib.ch).
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EMBL: M326061; AAB69155.1; -
DR DR

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DR PIR; B34611; B34611.
DR Genew; HGNC:8785; PDE6A.
DR MIM; 180071; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Plipase_HDC.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein;
KW Retinitis pigmentosa; Disease mutation.
FT INIT_MET 0
FT LIPID 856 856 FARNESYL (BY SIMILARITY).
FT VARIANT 343 343 S -> R (IN ARRP).
FT SEQUENCE 859 AA; 99503 MW; 983C361334D58414 CRC64;
SQ
Query Match 19.4%; Score 189; DB 1; Length 859;
Best Local Similarity 34.1%; Pred. No. 2.1e-08;
Matches 43; Conservative 29; Mismatches 52; Indels 2; Gaps 2;
QY 54 KDRFNDEIDKLTGYTKSLCMPISRSDDGEIIGVAQAINKIPGAPFDEDEKVMQMYL 113
DB 157 EDEHFCDFDVLTEYTKTKNILASPIMGCK-DVAILMAVNV-DGSHTKRDDEILLKYL 214
QY 114 PFCGTAISNAOLFASRKYEYSRALLVWVNDLFEQTDLEKIYKKIMHRAQTLLKCRC 173
DB 215 NFANILKMWLYSLYLNHCETRRGQILLWSGKVFEEITDIERQPHKALYTVRAFLNCDRY 274
QY 174 SVLLLE 179
DB 275 SVGLLD 280
RESULT 10
CNRB_HUMAN
ID CNRB_HUMAN STANDARD; PRT; 854 AA.
AC P35913; Q9BWH5;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase beta-subunit
DE (EC 3.1.4.17) (GMP-PDE beta).
CN PD6B OR PDEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93351644; PubMed=8394243;
RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Shmukler B.E.,
RA Terpugov B.E., Rakitina T.V., Atabekova N.V., Lipkin V.M.;
RT "The human rod photoreceptor cGMP phosphodiesterase beta-subunit.
RT Structural studies of its cDNA and gene.";
RL FEBS Lett. 327:275-278(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=93244036; PubMed=1338685;
RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Terpugov B.E.,
RA Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.;
RT "Structural studies of cDNA and the gene for the beta-subunit of cGMP
RT phosphodiesterase from human retina.";
RL Bioorg. Khim. 18:1551-1554(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
```

```
RX MEDLINE=92347868; PubMed=1322354;
RA Collins C., Hutchinson G., Kowbel D., Riess O., Weber B., Hayden M.R.;
RT "The human beta-subunit of rod photoreceptor cGMP phosphodiesterase:
RT complete retinal cDNA sequence and evidence for expression in brain.";
RL Genomics 13:698-704(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92066478; PubMed=1720239;
RA Weber B., Riess O., Hutchinson G., Collins C., Lin B., Kowbel D.,
RA Andrew S., Schappert K., Hayden M.R.;
RT "Genomic organization and complete sequence of the human gene encoding
RT the beta-subunit of the cGMP phosphodiesterase and its localisation to
RT 4p16.3.";
RL Nucleic Acids Res. 19:6263-6268(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 238-854 FROM N.A.
RC TISSUE=Retinal rod cell;
RX MEDLINE=96330350; PubMed=8768262;
RA Suslova V.A., Suslov O.N., Kim E.E., Lipkin V.M.;
RT "Organization of the gene for the beta-subunit of human photoreceptor
RT cyclic GMP phosphodiesterase.";
RL Bioorg. Khim. 22:256-263(1996).
RN [7]
RP VARIANT ADPR TYR-557.
RX MEDLINE=93350628; PubMed=8394174;
RA McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;
RT "Recessive mutations in the gene encoding the beta-subunit of rod
RT phosphodiesterase in patients with retinitis pigmentosa.";
RL Nat. Genet. 4:130-134(1993).
RN [8]
RP VARIANT CSNB3 ASN-258.
RX MEDLINE=94355978; PubMed=8075643;
RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
RT "Heterozygous missense mutation in the rod cGMP phosphodiesterase
RT beta-subunit gene in autosomal dominant stationary night blindness.";
RL Nat. Genet. 7:64-68(1994).
RN [9]
RP ERRATUM.
RX MEDLINE=95038845; PubMed=7951329;
RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
RL Nat. Genet. 7:551-551(1994).
RN [10]
RP VARIANT ARRP ASP-576.
RX MEDLINE=96129294; PubMed=8595886;
RA Danciger M., Blaney J., Gao Y.Q., Zhao D.Y., Heckenlively J.R.,
RA Jacobson S.G., Farber D.B.;
RT "Mutations in the PDE6B gene in autosomal recessive retinitis
RT pigmentosa.";
RL Genomics 30:1-7(1995).
RN [11]
RP VARIANTS ADPR LYS-166; HIS-212 AND HIS-228.
RX MEDLINE=96273603; PubMed=8698075;
RA Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Piriev N.I., Shih J.,
RA Jacobson S.G., Heckenlively J.H., Farber D.B.;
RT "Screening of the PDE6B gene in patients with autosomal dominant
RT retinitis pigmentosa.";
RL Exp. Eye Res. 62:149-154(1996).
RN [12]
RP VARIANT ARRP ARG-699.
RX MEDLINE=96140746; PubMed=8557257;
RA Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L.,
RA Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte R.,
RA Baiget M.;
RT "A novel mutation in exon 17 of the beta-subunit of rod
RT phosphodiesterase in two RP sisters of a consanguineous family.";
RL Hum. Genet. 97:35-38(1996).
RN [13]
RP VARIANT ARRP GLN-552.
```



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CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- DISEASE: IRISH SETTER DOGS AFFECTED WITH ROD/CONE DYSPLASIA (RCD1)
CC CONTAIN A NONSENSE MUTATION IN THE GENE THAT GIVES RISE TO A
CC PROTEIN OF 807 AA LACKING 49 AA IN THE C-TERMINAL.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z23014; CA80557.1; -
DR EMBL; L13262; AAA30882.1; ALT_SEQ.
DR PIR; S34290; S34290.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; vision; Prenylation; Lipoprotein; Membrane;
KW Disease mutation.
FT CHAIN 1 853 ROD CGMP-SPECIFIC 3',5'-CYCLIC
FT PROPEP 854 856 PHOSPHODIESTERASE BETA-SUBUNIT.
FT LIPID 853 853 REMOVED IN MATURE FORM (BY SIMILARITY).
FT SEQUENCE 856 AA; 98461 MW; AC9D03F64D1BA132 CRC64;
Query Match 18.8%; Score 183; DB 1; Length 856;
Best Local Similarity 33.6%; Pred. No. 6.7e-08;
Matches 45; Conservative 27; Mismatches 60; Indels 2; Gaps 2;
QY 46 LIQRTKTKRRFNDEIDKLTGYTKSLICMPIRSSDGEIIGVAQAINKIPGAPFTEDEKVMOMYL 105
Db 148 MNVQDVTECPHFSPFADELGYETRNILATPIMNGK-DVVAVIMALKL-DGPCFTFSED 205
QY 106 EKVQMVLPGFCIGAISSNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQ 165
Db 206 EDVLKYLNFCTLNKIYHLSYLNHCETRRGQVLLWSANKVFEELTDIERQFHKAFTYVR 265
QY 166 TLLKERCSCVLLLE 179
Db 266 AYLNCDRYSVGLLD 279
RESULT 12
CNRA_MOUSE STANDARD; PRT; 858 AA.
AC P27664;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
DE (EC 3.1.4.17) (GMP-PDE alpha).
GN PDE6A OR PDEA OR MPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Retina;
RC MEDLINE=91130581; PubMed=1847109;
RA Baehr W., Champagne M.S., Lee A.K., Pittler S.J.;

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RT "Complete cDNA sequences of mouse rod photoreceptor cGMP
RT phosphodiesterase alpha- and beta-subunits, and identification of
RT beta', a putative beta-subunit isozyme produced by alternative
RT splicing of the beta-subunit gene.";
RL FEBS Lett. 278:107-114 (1991)
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X60664; CAA43072.1; -
DR PIR; S13030; S13030.
DR MGD; MGI:97524; Pde6a.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; vision; Prenylation; Lipoprotein.
FT INIT_MET 0
FT LIPID 855 855 FARNESYL (BY SIMILARITY).
FT SEQUENCE 858 AA; 99515 MW; E29AG26B23F7DDAO CRC64;
Query Match 18.8%; Score 183; DB 1; Length 858;
Best Local Similarity 34.1%; Pred. No. 6.7e-08;
Matches 43; Conservative 27; Mismatches 54; Indels 2; Gaps 2;
QY 54 KDRRFNDEIDKLTGYTKSLICMPIRSSDGEIIGVAQAINKIPGAPFTEDEKVMOMYL 113
Db 157 EDEHCFDVFVNLEYQTKNILASPIIMNGK-DVVAVIMAVNKIDE-PHFTKRDEILLKYL 214
QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLKLCERC 173
Db 215 NFVNLIMKVFHLSYLNHCETRRGQVLLWSGSKVFEELTDIERQFHKAFTYVRFLNCDRY 274
QY 174 SVLLLE 179
Db 275 SVGLLD 280
RESULT 13
CNRA_CANFA STANDARD; PRT; 860 AA.
AC Q28263; Q29470;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Rod cGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
DE (EC 3.1.4.17) (GMP-PDE alpha).
GN PDE6A OR PDEA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
RN SEQUENCE FROM N.A.
RP

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RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=91015387; PubMed=1977087;
RA Bowes C., Li T., Danciger M., Baxter L.C., Applebury M.L.,
RT Farber D.B.;
RT "Retinal degeneration in the rd mouse is caused by a defect in the
RT beta subunit of rod cGMP-phosphodiesterase.";
RL Nature 347:677-680(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=91130581; PubMed=1847109;
RA Baehr W., Champagne M.S., Lee A.K., Pittler S.J.;
RT "Complete cDNA sequences of mouse rod photoreceptor cGMP
RT phosphodiesterase alpha- and beta-subunits, and identification of
RT beta', a putative beta-subunit isozyme produced by alternative
RT splicing of the beta-subunit gene.";
RL FEBS Lett. 278:107-114(1991).
CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
CC FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Beta';
CC are produced by alternative splicing.
CC -!- DISEASE: DEFECTS IN PDE6B ARE THE CAUSE OF RETINAL DEGENERATION.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.

Search completed: June 13, 2003, 15:47:44
Job time : 5.97722 secs

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or send an email to license@isb-sib.ch).

EMBL; X55968; CAA39439.1; ALT_SEQ.
EMBL; X60133; CAA42719.1; -
PIR; S13121; S13121.
MGB; MGI:97525; Pde6b.
InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Plpase_Hdc.
InterPro; IPR002073; PDEase.
InterPro; IPR001230; Prenyl_site.
Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 2.
PRINTS; PR00387; PDIESTERASE1.
SMART; SM00065; GAF; 2.
SMART; SM00471; HDC; 1.
PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; Vision; Prenylation; Lipoprotein; Membrane;
KW Alternative splicing.
FT CHAIN 1 853 ROD CGMP-SPECIFIC 3',5'-CYCLIC
FT PROPEP 854 856 PHOSPHODIESTERASE BETA-SUBUNIT.
FT LIPID 853 853 REMOVED IN MATURE FORM (BY SIMILARITY).
FT VARSPLOC 801 856 GERANYL-GERANYL (BY SIMILARITY).
FT CONFLICT 5 5 MISSING (IN ISOFORM 2).
FT CONFLICT 19 19 G -> E (IN REF. 2).
FT CONFLICT 49 50 S -> A (IN REF. 2).
FT CONFLICT 158 158 DV -> EL (IN REF. 2).
FT CONFLICT 176 176 T -> P (IN REF. 2).
FT CONFLICT 232 232 C -> L (IN REF. 2).
FT CONFLICT 236 236 R -> E (IN REF. 2).
FT CONFLICT 236 236 S -> G (IN REF. 2).
SQ SEQUENCE 856 AA; 98501 MW; 3677704D0C7496D1 CRC64;

Query Match 17.9%; Score 175; DB 1; Length 856;
Best Local Similarity 33.68; Pred. No. 3.le-07;
Matches 45; Conservative 23; Mismatches 64; Indels 2; Gaps 2;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 15:05:11 ; Search time 3005 seconds
(without alignments)
11199.408 Million cell updates/sec

Title: US-09-663-542-2

Perfect score: 2078

Sequence: 1 ggtccgagatgctgaagcag.....actaataactcgaggcatgc 2078

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	25.4	648	10	BB595063
2	473	22.8	724	10	BB639291
3	216.8	10.4	459	12	BC554930
4	184.8	8.9	501	13	BE672945
5	177	8.5	689	14	B0014209
6	166	8.0	472	17	AQ312583

7	155.4	7.5	884	9	AU079253
8	150.8	7.3	719	13	BI259167
9	150.8	7.3	941	13	BI259477
10	144.4	6.9	401	9	AI025081
11	142.8	6.9	744	14	BQ443199
12	141	6.8	644	13	BI255184
13	140.4	6.8	583	11	AK018833
14	140.4	6.8	591	11	AK005582
15	140.4	6.8	591	11	AK018851
16	138.2	6.7	639	17	AG065785
17	137.8	6.6	1067	13	BM450793
18	135.8	6.5	875	14	BQ928876
19	135.6	6.5	561	10	BE107807
20	132.8	6.4	905	17	CNS01E4X
21	130.2	6.3	800	12	BG214519
22	128.8	6.2	747	12	BG342646
23	127.2	6.1	876	13	BI733977
24	126.8	6.1	790	12	BG206143
25	123.4	5.9	516	12	BG087768
26	121.8	5.9	636	14	BM950937
27	121.8	5.9	987	12	BG171485
28	121	5.8	747	12	BG215073
29	119.8	5.8	738	13	BI736696
30	119.6	5.8	632	13	BI285638
31	119.2	5.7	782	13	AU120086
32	118.2	5.7	579	13	BI706530
33	118	5.7	506	13	BI326168
34	117.6	5.7	621	13	BI395052
35	116.2	5.6	573	13	BI708657
36	116.2	5.6	600	13	BI708675
37	116	5.6	798	14	BQ720185
38	115.6	5.6	655	14	BQ572379
39	115.2	5.5	1004	14	BM923051
40	114.8	5.5	322	10	AW158676
41	114.8	5.5	607	10	AW640964
42	114.8	5.5	616	14	BQ400425
43	114.6	5.5	690	9	AI134280
44	114.2	5.5	766	12	BG213437
45	114	5.5	608	10	BE532887

ALIGNMENTS

RESULT 1

BB595063

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BB595063

musculus

BB595063

BB595063

EST

house mouse

Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 648)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

On Nov 30, 2000 this sequence version replaced gi:11491665.

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

On Nov 30, 2000 this sequence version replaced gi:11491665.

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

648 bp mRNA linear EST 26-OCT-2001
RIKEN full-length enriched, adult male corpus striatum Mus
cDNA clone C030004B19 5', mRNA sequence.

AU079253 AU079253
BI259167 602970010
BI259477 602970109
AI025081 ov40a11.x
BQ443199 UI-M-EV0-
BI255184 602977479
AK018833 Mus muscu
AK005582 Mus muscu
AK018851 Mus muscu
AG065785 Pan trogl
BM450793 AGENCOURT
BQ928876 AGENCOURT
BE107807 UI-R-CAO-
AI140098 Anopheles
BG214519 RST34162
BG342646 602374642
BI733977 603355506
BG206143 RST25578
BG087768 H3144G02-
BM950937 UI-M-EGO-
BG171485 602322019
BG215073 RST34731
BI736696 603360282
BI285638 UI-R-DDO-
AU120086 AU120086
BI706530 fq07b01.y
BI326168 fp86g03.y
BI395052 pqln.pk0
BI708657 fq08e12.y
BI708657 fq09e11.y
BQ720185 AGENCOURT
BQ572379 UI-M-FD0-
BM923051 AGENCOURT
AW158676 za44b04.x
AW640964 cm01h02.w
BQ400425 NISCmp09
AI134280 GH11694.5
BG213437 RST33043
BE532887 601234782


```
Query Match      10.4%; Score 216.8; DB 12; Length 459;
Best Local Similarity 77.4%; Pred. No. 2.1e-51;
Matches 263; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1690 TAATGACAGCCTGTGACCTTGAGCGGTGACCAACCGTGGGAGATCTCCAGACAGGTGG 1749
Db 1 TAATGACAGCGTGTGACCTTGAGCGGTGACCAACCGTGGGAGATCTCCAGACAGGTGG 60

QY 1750 CAGAAGCTTGTAAACAGTGTGCTTTCGAACAGGAGATCGGAGAGATAGAGCTCAAC 1809
Db 61 CTGAGTTGGTACACAGTGTGCTTTCGAACAGGAGATCGGAGAGATAGAGCTCAAC 120

QY 1810 TCATCCCTTCAGCAATTTTGTATCGGAACCGAAGGATGAATCGCTCGTTTCAACTGG 1869
Db 121 TGACACCTTCAGCCATTTTGTATAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 180

QY 1870 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1929
Db 181 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 1930 TGAAGCCGATGCTAGATTCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1989
Db 241 TTAAGCCCTATGTTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 1990 AACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2029
Db 301 AACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340

RESULT 4
LOCUS B1672945
DEFINITION ft39g12.y1 Gong zebrafish testis Danio rerio cDNA clone 5153110 5'
similar to TR:Q9WJ79 Q9WJ79 CG10231 PROTEIN. ; mRNA sequence.
ACCESSION B1672945
VERSION B1672945.1 GI:15588329
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
REFERENCE Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
WashU zebrafish EST Project 1998
Unpublished (1998)
Other ESTs: ft39g12.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
Seq primer: T3 ET from Amersham
High quality sequence stop: 393.
Location/Qualifiers
1..501
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5153110"
/clone.lib="Gong zebrafish testis"
/sex="male"
/dev_stage="4-5 month"

FEATURES
source
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolated from
the testes of 31 male adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excision to pBluescript SK- following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
```



```
source
1. .689
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5833095"
/clone_lib="NCI_CGAP_EDI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/Note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI_CGAP_EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CCS. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (GT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB=UI-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAGGCT"

BASE COUNT      182 a 126 c 125 g 253 t      3 others
ORIGIN

Query Match      8.5%; Score 177; DB 14; Length 689;
Best Local Similarity 58.8%; Pred. No. 9.6e-40;
Matches 322; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

QY 1362 CTGTGTCATGACCTCGACACGAGGAGCAACCAATGCTTCCAAAGCTAAGAGTGCTCT 1421
   || || || || || || || || || || || || || || || || || || || || ||
Db 684 CTAAGCCACGATNGGATCACCGTGGTGTGATRACTNTACATACCGGAAGTGAACAT 625

QY 1422 GCCCTGGCCCAACTCTATGGAACTCTGCTACCTGGAGCATACACATTTCAACACGCC 1481
   || || || || || || || || || || || || || || || || || || || || ||
Db 624 CCACCTGGCCAGCTTTACTG---CCATTCAATCATGGAACACCATCAITATGACCAGTGC 568

QY 1482 GTGATGATCTTCAAGAGGAGGTGACAAATATCTTTGCTAACCTGCTCTCCAAAGAAAT 1541
   || || || || || || || || || || || || || || || || || || || || ||
Db 567 GTATGATCTTATAGTCCAGGCATCAGATCTCTAGTGGCCTCTCCATTTGAAGAATAT 508

QY 1542 AGTGACCTTATGACGCTTTTGAAGCAGTCAATATTTGGCAACAGACCTCACGCTGTACTTT 1601
   || || || || || || || || || || || || || || || || || || || || ||
Db 507 AAGACCAGCTTGAATAATCAAGCAAGCTATTTTAGCTACAGACCTAGCACTGTACATT 448

QY 1602 GAGAGGAACTGAATCTTTTGAACCTTCTAGTAAAGAGAGATAGGATTTGAACATCAA 1661
   || || || || || || || || || || || || || || || || || || || || ||
Db 447 AAGAGCGGAGGAGAAATTTTGAACCTTATAAGAAAAATCAATTTCAATTTGGAAGATCCT 388

QY 1662 AACCATCTGATATATTTTCGATCAATGTTAATGACAGCCTGTGACCTTTGGAGCGGTGACC 1721
   || || || || || || || || || || || || || || || || || || || || ||
Db 387 CATCAAAAGGAGTTGTTTTCGCAATGCTGATGACAGCTTGTGATCTTCTTGCATTTACA 328

QY 1722 AAACCGTGGGAGATCTCCAGACAGGTGGCAAGACTTGTAAACAGTGTACTTCTTCGAACAA 1781
   || || || || || || || || || || || || || || || || || || || || ||
Db 327 AAACCTGGCCTATTCAACAACGGATAGCAGAACTTTGTAGCAACTGAATTTTTCATCAA 268

QY 1782 GGAGATCGGAGAGATTTAGAGCTCAAACTCACTCCTTCAGCAATTTTTCAGCGAACCGG 1841
   || || || || || || || || || || || || || || || || || || || || ||
Db 267 GGAGACAGAGAGAGAAAGAACTCAACATAGAACCCACTGTATCTAATGAAAGGGAGAG 208

QY 1842 AAGGATGAATGCTCGCTGCTGCACTGAGTGGATTTGATAGCATCTGCATGCTTTGTAT 1901
   || || || || || || || || || || || || || || || || || || || || ||
Db 207 AAAACAAAATCCCAAGTATGCAAGTTGGGTTTCATAGATGCCATCTGCTTGCACTGTAT 148

QY 1902 CAGGCACT 1909
   || || ||
Db 147 GAGGTATT 140
```

```
RESULT 6
AQ312583
LOCUS
DEFINITION
  RPC111-95E23.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-95E23,
  DNA sequence.
ACCESSION
  AQ312583
VERSION
  AQ312583.1 GI:4044247
KEYWORDS
  GSS.
SOURCE
  human.
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 472)
  Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
  Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
  Use of human BAC End Sequences for Sequence-Ready Map Building
  Unpublished (1998)
  JOURNAL
  Other_GSSs: RPC111-95E23.TV
  CONTACT: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel.: 301 838 0200
  Fax: 301 838 0208
  Email: hbeetigr.Org
  Clones are derived from the human BAC library RPC1-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
  Research Genetics (info@resgen.com). BAC end search page:
  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
  Seq primer: SP6
  Class: BAC ends.
  Location/Qualifiers
    1..472
      /organism="Homo sapiens"
      /db_xref="GDB:7536214"
      /db_xref="taxon:9606"
      /clone="RPC1-11-95E23"
      /clone_lib="RPC1-11"
      /sex="Male"
      /cell_type="Lymphocytes"
      /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
      RPC11 Human Male BAC Library"
BASE COUNT      169 a 72 c 97 g 134 t
ORIGIN

Query Match      8.0%; Score 166; DB 17; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.2e-36;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAGATGCTGAAGCAGGCAAGAACCTTTATTTCAGAAATGCTCAGTGCCACACAGTGG 65
   || || || || || || || || || || || || || || || || || || || || ||
Db 33 GAGATGCTGAAGCAGGCAAGAACCTTTATTTCAGAAATGCTCAGTGCCACACAGTGG 92

QY 66 AAAAGGTGAAAATCACAAGACTGTGTCAAAATCTCTGGGGCCTCTTTGGCTGAAAAACAG 125
   || || || || || || || || || || || || || || || || || || || || ||
Db 93 AAAAGGTGAAAATCACAAGACTGTGTCAAAATCTCTGGGGCCTCTTTGGCTGAAAAACAG 152

QY 126 GAAAGACACAGGATTTCTTATACAGAGGCAACAAAAACAAAGG 171
   || || || || || || || || || || || || || || || || || || || || ||
Db 153 GAAAGACACAGGATTTCTTATACAGAGGCAACAAAAACAAAGG 198

RESULT 7
AU079253
LOCUS
DEFINITION
  AU079253 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-4049
  5', mRNA sequence.
ACCESSION
  AU079253
VERSION
  AU079253.1 GI:6084008
KEYWORDS
  EST.
SOURCE
  house mouse.
```


BASE COUNT	228 a	283 c	229 g	201 t	
ORIGIN					
Query Match	7.3%	Score 150.8;	DB 13;	Length 941:	
Best Local Similarity	54.0%;	Pred. No. 4.7e-32;			
Matches 355;	Conservative	0;	Mismatches 297;	Indels 6;	Gaps 2;
Qy	1140	CTCCGGATGTTTCATGGAGCTGGGGATGGTTACAGAAATTTAAAATTGACTATGAGACACTG	1199		
Db	4	CTGAGCATGCTGAGGACATGAATTTTCATCAACAACATACAAAATTTGATCTCCCGACCCCT	63		
Qy	1200	TGTAGTGGCTTTTGACAGTGGAGAAACACTATCGGATGTTCTATACCACAACCTGGAGA	1259		
Db	64	GCCCGTTCTGTTTGATGTTGAAGAGGGCTACGGGATCCCCCTACCAACAATGGATG	123		
Qy	1260	CATGCGCTTCAACGTGTCTAGCTGATGTTTCGGCATGTTAAACCACCTGCTGGGTTTCAAGAC	1319		
Db	124	CAGCGCTTTTCTGCTCCCACTTCTGTACTGCTCTACAAAGAACCTTGGAGCTCACCAAC	183		
Qy	1320	ATTCTGACGAGTGGAAATTTTAGCGGTGATTTCTGGGATGCGCTGTGTCATGACCTCGAC	1379		
Db	184	TACTCTGAGGACATCGAGATCTTTGGCTTGTTTATTTCCTGCAATGTCTATGACCTGGAC	243		
Qy	1380	CACAGGGGAACCAACATGCTTCCAAAGCTTAAGAGTGGCTCTGCGCTGGCGCCAACTCTAT	1439		
Db	244	CACAGAGGCACAAACAACTCTTCCAGTGGCGCTCGAAATCTGTGCTGGCTGCGCTCTAC	303		
Qy	1440	GGAACTCTG ---CTACCTTGGAGCATACACATTTTCAACCAGCGGTGATGATCCTTCAA	1496		
Db	304	AGCTCTGAGGGCTCCCGTCATGGAGGACACACATTTGCTCAGGCCATCGCCATCCTCAAC	363		
Qy	1497	AGTGAGGGTCACAATATCTTTTGCTTAACCTCTCTCCAAAGGAATATAGTGACCTTATGCGAG	1556		
Db	364	ACCCAGGCTGCACACATCTTTTGATCATTTCTCCGGGAAGCACTATCAGCGCATGCTGGAT	423		
Qy	1557	CTTTTGAAGCAGTCAATATTTTGGCAACAGACCTCACGCTGTACTTTGAGAGGAGAACTGAA	1616		
Db	424	CTGATGCGGACATCATCTTTGGCCACAGACCTTGCGCCACCATCTCCGCATCTTCAAGGAC	483		
Qy	1617	TTCTTTGAACTTGTCTAGTAAAGGAGAAATACGATTGGAAACATCAAAAACCATCTGATATA	1676		
Db	484	CTCCAGAAGATGGC ---TGAGGTGGGTACGACCGGAACAAACAGCAGCACACAGACTT	540		
Qy	1677	TTTTCGATCAATGTTAATGACAGCTCTGTGACCTTTGGAGCCGTGACCAAAACCGTGGAGATC	1736		
Db	541	CTCCTCTGCGCTCTCATGACCTCTCTGTGACCTCTCTGACCAACCAAGGGCTGGAAGACT	600		
Qy	1737	TCCAGACAGTGGCAGAACCTTTGTAAACCAAGTGGATTCTTTCGAACACAGGATCGGGAGA	1794		
Db	601	ACCAAGAAGATCGCGAGCTGATCTACAAAGAATTTCTTCCAGGAGACCTTGGAGA	658		

RESULT 10
AI025081/c
LOCUS AI025081 401 bp mRNA linear EST 27-AUG-1998
DEFINITION ov40all.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639772 3' similar to TR:Q28156 Q28156 CGMP-SPECIFIC PHOSPHODIESTERASE. 1; mRNA sequence.

ACCESSION	A1025081
VERSION	A1025081.1
KEYWORDS	GI:3240694
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1 (bases 1 to 401)
COMMENT	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: coapbs-r@mail.nih.gov cnaa.lib@nci.nih.gov

Email: cgap@remail.nhn.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Ronaldo

Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 370.

FEATURES

Location/Qualifiers
1. .401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1639772"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTACCATCTGAAGTGGGCGGCGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 123 a 89 c 63 g 126 t
ORIGIN

Query Match 6.9%; Score 144.4; DB 9; Length 401;

Best Local Similarity 96.1%; Pred. No. 2e-30;

Matches 148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 409 AAGAGCAGAGCTTGGTAGAGTGGTTAATGACCTTTTGAAGAACAGACTGACCTGG 468

Db 221 AAGAGCTGGTTGGTGGTAGAGTGGTTAATGACCTTTTGAAGAACAGACTGACCTGG 162

QY 469 AGAAAATTGTCAGAAAATAATGCATCGGCGCCCAACTCTGCTGAATGTGAGCGCTGT 528

Db 161 AGAAAATTGTCAGAAAATAATGCATCGGCGCCCAACTCTGCTGAATGTGAGCGCTGT 102

QY 529 CTGTTTTACTCTAGAGGACATCGAATCACCAGT 562

Db 101 CTGTTTTACTCTAGAGGACATCGAATCACCAGT 68

RESULT 11

BQ443199

LOCUS

DEFINITION

UI-M-EV0-bxg-k-19-0-UI.r1 NIH_BMAP_EV0 Mus musculus cDNA clone

IMAGE:5707914 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

744 bp mRNA linear EST 29-MAY-2002
BQ443199
UI-M-EV0-bxg-k-19-0-UI.r1 NIH_BMAP_EV0 Mus musculus cDNA clone
IMAGE:5707914 5', mRNA sequence.
BQ443199
EST.
BQ443199.1 GI:21246311
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 744)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

FEATURES

Location/Qualifiers
1. .744
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5707914"
/clone_lib="NIH_BMAP_EV0"
/tissue_type="whole Brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP); 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 183 a 227 c 156 g 175 t
ORIGIN

Query Match 6.9%; Score 142.8; DB 14; Length 744;

Best Local Similarity 53.1%; Pred. No. 8.6e-30;

Matches 347; Conservative 0; Mismatches 300; Indels 6; Gaps 2;

QY 1107 TCTCTGCGATGGTATGCCATGATCACAGCTGCTCCGGATGTTTCAGAGCTGGGATG 1166

Db 88 TCTCTGCGATGGAGCAGACACTCTTATGGCATCTCGAGCATGCGAAGACATGAATTC 147

QY 1167 GTACAGAAATTTAAATTCAGTATGAGACACTGCTAGTGGTGGCTTTTGACAGTGAGAAA 1226

Db 148 ATCAATTAATACAAAATGACTGCCCAACTCTGGCCCGATCTGCGCTGATGGTGAAGAAA 207

QY 1227 AACTATCGGATGTTCTTATACCAACATCGAGACATGCCCTTCAACGTGTCTACGTGATG 1286

Db 208 GGCTACCGGGATCCACCTTACCACACTGGATGCGAGCTCTCTCTCTCATTTTTCG 267

QY 1287 TTGCGGATCTTACCACTGCTGGGTTTCAAGACATTTTGACCGAGGTGGAAATTTTAGCG 1346

Db 268 TACCTGCTCTACAAGAAATCTGGAGCTCTCCAACTACCTCGAGGACATCGAGATCTTTGCA 327

QY 1347 GTGATTGCGGATGCTGTCTGATGACCTCGACCAGGGGACCAACAATGCCTTCCAA 1406

Db 328 TTGTTTATTTCTTGGCATGTCTGATGACCTGGAGGACAGAGGACCAACAACCTCTCCAG 387

QY 1407 GCTAAGAGTGGCTGCTGCCCTGGCCCAACTCTATGGAACCTCTG---CTACCTTTGAGCAT 1463

Db 388 GTGGCTCGAATCTGTGCTGGCCGCACTCTACAGCTCAGAGGGCTCTCTCATGGAGAGG 447

QY 1464 CACCAATTTCAACACGCGCTGATGATCTTTCAAGTGAAGGTGACAAATATCTTTGTGAAC 1523

Db 448 CACCCTTTGCTCAAGCCATTTGCTATCTTCAACACCGGCTGCAATATCTTTTGACCA 507

QY 1524 CTTGCTCTCAAGGAATATAGTACCTTATGACCTTTTGAACGAGTCAATATTTGCAACA 1583

Db 508 TTCTCTGGGAAGACTATCAGCGCATGCTGAGGACCTGATGAGGACATCATCTTTGGCTACA 567

QY 1584 GACCTCACCTCTACTTTTGAGAGGAGAACTGAATTTTGAACCTTGTCTAGTAAGAGAGAA 1643

Db 568 GACCTGGCACACCACTCCGCTCTTCAAGGACCTCCCAAGATGCG---TGAAGTGGGT 624

QY 1644 TAGGATTGGAACATCAAAACCACTGATATATTTTTCGATCAATGTTAATGACAGCTGT 1703

Db 625 TATGACCGAACAACAGGCAACACAGGCTTCTTCTGCTCTCTATGACCTCTCTGT 684

Db 302 GAATCTGTCTGGCTGGCTCTACAGCTCTGAGGGCTCCGTATGAGAGGACCACCTT 361
 QY 1472 CAACCACGGCGTGATGATCTTCAAAGTGAGGGTCACAATATCTTTCTTAACCTGTCTC 1531
 Db 362 TGCTCAGGCCATCGCCATCTCAACACCCACGGCTGCAACATCTTTGATCATTTCTCCG 421
 QY 1532 CAAGGATATAGTACCTTATGAGCTTTTGAAGCAGTCAATATTGGACACAGACCTCAC 1591
 Db 422 GAAGGACTATCAGCGCATGCTGGATCTGATCGGGGACATCATCTTGGCCACAGACCTGC 481
 QY 1592 GCTGTACTTTGAGGAGAACTGAATCTTTGACTTTGTCAGTAAAGGAAATACGATTG 1651
 Db 482 CCACCTCTCCGATCTTCAAGGACCTCCAGAAAGATGG---CTGAGGTGGCTACGACCG 538
 QY 1652 GAACTCAAAAACCATCGTGATATATTTCGATCAATGTTAATGACAGCCTGTGACCTTGG 1711
 Db 539 AACAACAAGCAGCACACAGACTTCTCTCTGCTCCTCATGACCTCTCTGTGACCTCTC 598
 QY 1712 AGCCGTGACCAACCGTGGGAGATCTCCAGACAGGTGGCGAACT 1756
 Db 599 TGACCAGACCAAGGCTGGAAGACTACGAGAAGATCGCGGAGCT 643

RESULT 13
 LOCUS AK018833
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700008G06:cytochrome c, testis, full insert sequence.
 ACCESSION AK018833
 VERSION AK018833.1 GI:12858775
 KEYWORDS HPC; CAP trapper.
 SOURCE Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library
 clone:1700008G06.
 ORGANISM Mus musculus
 'Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,I., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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 4 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gotojori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 10:41:07 ; Search time 489 seconds
(without alignments)
9569.842 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2078	100.0	2078	22	AAF62311 Human cyclic nucle
2	2056.4	99.0	3507	22	AAH46709 Human type 11 phos
3	1891.8	91.0	4476	22	AAH46708 Human type 11 phos
4	1734.8	83.5	2994	22	AAH78232 Nucleotide sequenc
5	1684	81.0	3492	22	AAH46710 Rat type 11 phosph
6	1551.4	74.7	4170	22	AAH46742 Rat type 11 phosph
7	1503.8	72.4	1784	21	AAA45972 Human cyclic nucle
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9	1045.6	50.3	1982	21	AAA49973 Human cyclic nucle

10	388.8	18.7	.426	24	AAZ28571 Human PDE-like enz
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14	356.6	17.2	2645	16	AAQ79713 Cyclic guanosine m
15	356.6	17.2	2645	20	AAQ99393 Human cGMP-binding
16	355	17.1	2499	21	AAZ95233 Human phosphodiester
17	355	17.1	3381	21	AAA14957 DNA encoding a PDE
18	345.2	16.6	1982	16	AAQ79705 Cyclic guanosine m
19	345.2	16.6	1982	19	AAV05066 Bovine phosphodies
20	345.2	16.6	1982	20	AAQ99383 Human cGMP-PDE cDNA
21	343.6	16.5	4426	19	AAV09064 Bovine cGMP-bindin
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25	224.2	10.8	3699	23	ABL13737 Drosophila melanog
26	219.2	10.5	2406	21	AAQ9590 Human phosphodiester
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28	219.2	10.5	2798	21	AAZ36964 DNA encoding a hum
29	219.2	10.5	3631	22	ABA03665 Human PDE10A cDNA.
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41	216.6	10.4	3789	19	AAV48204 Cyclic-GMP-stimula
42	216.6	10.4	3789	19	AAV54761 Bovine brain cGMP-P
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44	216.6	10.4	3789	21	AAZ90380 Bovine brain cGMP-P
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ALIGNMENTS

RESULT 1

AAF62311

ID AAF62311 standard; cDNA; 2078 BP.

XX

AC AAF62311;

XX

DT 06-JUN-2001 (first entry)

XX

DE Human cyclic nucleotide phosphodiesterase PDEXV coding sequence.

XX

KW Human; cyclic nucleotide phosphodiesterase; PDEXV; sexual dysfunction;

KW cardiovascular disease; gastrointestinal disorder; corpus cavernosum;

KW kidney; liver; skeletal muscle; testis prostate; spleen; ss.

XX

OS Homo sapiens.

XX

FH Key.

FT CDS

FT Location/Qualifiers

FT 9..2063

FT /*tag= a

FT /product= "PDEXV"

XX

EP1085089-A2.

XX

PD 21-MAR-2001.

XX

PF 14-SEP-2000; 2000EP-0307981.

XX

PR 17-SEP-1999; 99GB-0022124.

XX

PA (PF12) PFIZER LTD.

XX

PA (PF12) PFIZER INC.

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Qy	1801	AGCTCAAACTCACTCCTTTCAGCAAAATTTTGATCGGAACCGAAGATGAACCTGCCGCT	1860
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RESULT 4
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AC AAH78232;
XX
DT 26-NOV-2001 (first entry)
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DE Nucleotide sequence of a human phosphodiesterase polypeptide.
XX
KW Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;
KW nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;
KW osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;
KW Parkinson's disease; dementia; infectious disease; malignant tumour; ss.
XX Homo sapiens.
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XX PN WO200166716-A1.
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XX PD 13-SEP-2001.
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XX PF 06-MAR-2001; 2001WO-JP01720.
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XX PR 10-JUL-2000; 2000JP-0208610.
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XX PA (KYOW) KYOWA HAKKO KOGYO KK.
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AC AAH46710;
XX 19-SEP-2001 (first entry)
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XX Rat; type 11 phosphodiesterase; pDE11; signal transduction;
KW selective inhibition; ds.
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XX WO200146436-A1.
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XX 28-JUN-2001.
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XX 22-DEC-2000; 2000WO-JP09118.
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XX 22-DEC-1999; 95JP-0364866.
PR 01-JUN-2000; 2000JP-0163875.
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XX (TANA) TANABE SEIYAKU CO.
XX
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX
XX WPI: 2001-418074/44.
DR P-PSDB; AAG62679.
XX
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy
XX
XX Claim 7; Page 51-55; 77pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (pDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a coding sequence of the invention.
XX
XX Sequence 3492 BP; 963 A; 792 C; 865 G; 872 T; 0 other;
SQ
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Best Local Similarity 88.5%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 235; Indels 3; Gaps 1;
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DB 238 GAGATGCTGAGCAGGCGAAGAGATTTTCATTCAGAAATGTGCGCAGTGCCACACAGTGG 297
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QY 246 AGCAGTGATGGGAGATTTATGGTGGCCCAAGCGATTAATTAAGATTCCTGAAGAGCT 305
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DB 838 AGTGGGACGGGAGAACAGTTTCAAGAAAGTGTGGAGAACTCATCTTACTCCGACTGG 897
QY 666 CTAATAAATAACAGCAITGCTGAGCTGGTGTCTTCAACAGGCGCTTCCAGTGAACATCAGT 725
DB 898 CTGATAAATAACAGTATCGCTGAGCTGGTGTCTTCCGACAGGCGCTTCTCTGTAATCTCAGC 957
QY 726 GATGCTACCAAGGATCCGCGCTTTGATGCAGAGGACAGACAGATATCTGTTTTCACATA 785
DB 958 GATGCTACCAAGGACCGCTTTGACGCTGAGGCTGACGATATCTGGCTTTCATATA 1017
QY 786 AGATCTGTTCTTTGTCCTCTATTTGGAATAGCAACACCAAAATATTTGGAGTGCCTCAA 845
DB 1018 AGATCTGTTCTGTCCTCTATTTGGAACACCAACCAAAATATTTAGGGGTCCCTCAA 1077
QY 846 GTGTTAAACAGACTTGTGGGAAACCTTTTGTATGATGCAGATCAACAGCTTTTTCAGGCT 905
DB 1078 GTGCTGAACAGACTCGATGGGAAACCTTTTGTATGATGCTGACCAAGGCTTTTTCAGGCT 1137
QY 906 TTTGTCATCTTTTGTGGACTTGGCATCAACACAAATATATGATCAAGTGAAGAAG 965
DB 1138 TTTGTCATCTTTTGTGGCTTGGTATTAACAACAGCATATGATGACCAAGTGAAGAAG 1197
QY 966 TCCTGGGCCAACAGCTCTGTGCTCTGTATGTGCTCATACCATGCAACATGTTTCAAAA 1025
DB 1198 TCCTGGGCCAACAGCTCTGTGCTCTGTATGTGCTCTCTACCAAGGCTGTTTCCAG 1257
QY 1026 GCTGAAGTTGACAGTTTAAAGCAGCCCAACATCCCTCTGGTGTCAAGAACTTGCCTCAT 1085
DB 1258 GCTGAAGTTGACAGTTTAAAGCAGCCCAACATCCCTCTGGTGTCAAGAACTTGCCTCAT 1317
QY 1086 GACATTCATTTTGTGACTTTTCTCTGACGTTTGTATGCGATGATCAGAGCTGCTCTCCGG 1145
DB 1318 GACATTCATTTTGTGACTTTTCCCTTGTATGTCATGATCAGAGCTGCTCTACGG 1377
QY 1146 ATGTTCTGAGCTGGGATGTACAGAAATTTTAAATTTGACTATGAGACACTGTGTAGG 1205
DB 1378 ATGTTCTGAGCTGGGATGTACAGAAATTTTAAATTCGACTATGAGACCTGTGTGAGG 1437
QY 1206 TGGCTTTTTCAGAGTGAAGAAAAATTCGGATGTTTCTATACCAACCTTGGAGACATGCC 1265
DB 1438 TGGCTTCTGACAGTAAGGAAAAATTCGGATGTTTCTTACCAACCTTGGAGACATGCC 1497
QY 1266 TTCAACGTGTGTACGCTGATGTTCCGATGTTTAAACCACTGCTGGGTTTCAAGACATCTG 1325
DB 1498 TTCAACGTGTGTACGCTGATGTTTCCCATGCTTAACCTGCTGCTGTTTCAAGAGATCTG 1557
QY 1326 ACCGAGGTGGAAATTTTACGCTGATTTAGCGTGTGTTAGCGTGTGTCATGACCTCGACACAGG 1385
DB 1558 ACCGAGGTGGAAATTTTACGCTGATTTAGCGTGTGTTAGCGTGTGTCATGACCTCGACACAGG 1617
QY 1386 GGAACCAACAATGCCCTTCCAAAGTAAAGATGGCTCTGCCCTGGGCCCAACTCTATGGAACC 1445

Db 1618 GGAACCAACAAATGCGCTTCAAGCTAAGAGTGAAGTCTGCACTGGCCAGCTCTATGGGACC 1677
Qy 1446 TCTGTACCTTGGAGCATCACCATTTCACACCGCGTGATGATCCTTCAAGTCAAGGT 1505
Db 1678 TCAGGACCTTAGAGCATCACCATTTCACACCGCGTGATGATCCTTCAAGTCAAGGT 1737
Qy 1506 CACAATATCTTTGCTAACTGCTCTCCCAAGGAATATAGTACCTTTATGACAGCTTTTGAAG 1565
Db 1738 CACAACATCTTTGCTAACTGCTCTCCCAAGGAATATAGTACCTTTATGACAGCTTTTGAAG 1797
Qy 1566 CAGTCAATATGCGCAACAGACCTCAGCTGTACTTTGAGAGAGAACTGAATCTTTGAA 1625
Db 1798 CAGTGCATACTACCACTCAGCTCAGCTGTACTTTGAGAGAGAACTGAATCTTTGAA 1857
Qy 1626 CTTGTCAGTAAAGAGAGATACGATTGGGAACATCAAAACCAATCGTGATATATTCGATCA 1685
Db 1858 CTTGTCAGTAAAGAGAGATGATTTGGAGCATCACAAGTCAACCGGATGTTGTCGATCA 1917
Qy 1686 ATGTTAATGACAGCCTGTGACCTTGGAGCGGTGACCAACCGTGGAGATCTCCAGACAG 1745
Db 1918 ATGTTAATGACAGCTGTGACCTTGGAGCGGTGACCAACCGTGGAGATCTCCAGACAG 1977
Qy 1746 GTGGCAGAACTGTACACAGTGTCTTCGAAAGAGAGATCGGGAGAGATTAGAGCTC 1805
Db 1978 GTGGCTGAACCTGTCCAGCAGGAGTTCTTCGAAACAGAGAGATCGGGAGAGTCCGGAATC 2037
Qy 1806 AAACCTCACTCTCTCAGCAATTTTCATCGGAACCGGAAGGATGAACCTCGCTGCTGCAA 1865
Db 2038 AGCTCAACCCCTCTGCTATTTTCACCGGAACCGGAAGATGAGCTGCCCTGCGCTGCA 2097
Qy 1866 CTTGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1925
Db 2098 CTTGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2157
Qy 1926 AAACCTGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1985
Db 2158 AAACCTGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2217
Qy 1986 CAAAACAGCTCTGCGCTCAACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2042
Db 2218 CAAAACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Qy 2043 GCCAAGGAG 2078
Db 2278 GCCGAG 2313

RESULT 6
AAH46742
ID AAH46742 standard; DNA; 4170 BP.
AC AAH46742;
XX
DT 19-SEP-2001 (first entry)
DE Rat type 11 phosphodiesterase coding sequence SEQ ID NO: 38.
XX
KW Rat: type 11 phosphodiesterase; PDE11; signal transduction;
XX selective inhibition; ds.
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT 169..2976
FT /*tag= a
FT /product= "PDE11"
XX

WO200146436-A1.
XX
XX 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-JP09118.

XX 22-DEC-1999; 99JP-0364866.
PR 01-JUN-2000; 2000JP-0163875.
XX
PA (TANA) TANABE SEIYAKU CO.
XX
PI Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX
DR WPI: 2001-418074/44.
DR P-PSDB; AAG62680.
XX
PT Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy
XX
PS Claim '7; Page 64-69; 77pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms. In screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a coding sequence of the invention.
XX
SQ Sequence 4170 BP; 1100 A; 1004 C; 1067 G; 999 T; 0 other;
Query Match 74.7%; Score 1551.4; DB 22; Length 4170;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 216; Indels 3; Gaps 1;
Qy 169 AGGATCGACGATTCAATGATGAAATCGAAGCTGACTGGATACAAGCAAAATCATAT 228
Db 1079 AGGACCGAAGATTCAATGATGAAATCGAAGCTGACTGGATACAAGCAAAATCATAT 1138
Qy 229 TGTGCATGCTTATCCGAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 288
Db 1139 TGTGCATGCTTATCCGAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1198
Qy 289 AGATTCTGAGGAGCTCCATTACTGAAGATGATGAAGAATGATGATGATGATGATGATGATGAT 348
Db 1199 AGTTCTCTGAGGCTGCTCCATTTACAGAAGCAGCAGAAAGATTTATGATGATGATGATGAT 1258
Qy 349 CATTTTGTGGAATCGCCATATCAACCTCAGCTCTTTGCTGCTCAGGAAAGCAATATG 408
Db 1259 CATTTCTGGCATCGCCATATCTAATGCTAGCTCTTCGCGGCTTCGAGGAAAGCAATATG 1318
Qy 409 AAAGAAGCAGAGCTTTGCTAGAGGTGTTAATGACCTCTTTGAAGAACAGACTGACCTGG 468
Db 1319 AAAGAAGTAGGCGCTTCTGCGAGCTGTTCAATGACCTCTTTGAAGAACAGACTGACCTGG 1378
Qy 469 AGAAATTTCAAGAAATATATGATCGGGCCCAAACTCTGCTGCTGCTGCTGCTGCTGCTGCT 528
Db 1379 AAAAGATTGTCAAGAAATATATGATCGGGCCCAAACTCTGCTGCTGCTGCTGCTGCTGCT 1438
Qy 529 CTGTTTCTACTCTAGAGGACATCGAATCACCAGTGTGAATTTACCAAAATCTTTTCAAT 588
Db 1439 CCGTTTCTACTCTAGAGGACATCGAATCACCAGTGTGAATTTACCAAAATCTTTTCAAT 1498
Qy 589 TGATGTCCCAAACTGCGCTGCTGATGCTGAGAACAGTTCCTCAAGAAAGCATGAGAAAT 648
Db 1499 TGATGTCCCAAACTGCGCTGCGGACGCGGAGAACAGTTCCTCAAGAAAGCATGAGAAAT 1558
Qy 649 CATCATACTCGGACTGCTTAATAATACACAGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 708
Db 1559 CATCTTACTCGGACTGCTTAATAATACACAGTATCATGCTGCTGCTGCTGCTGCTGCTGCT 1618
Qy 709 TTCCAGTGAACATCAGTGTGCTTACCAGGATCGCGCTTTGATGACAGAGCACCAGCA 768
Db 1619 TTCTGTGAATGTCAGCGATGCCCTTACCAGGACCCAGCTTTGAGCTGAGCTGAGCTGAGCA 1678
Qy 769 TATCTGTTTTTCACATAAGATCTGTTCTTTGTGCTCCTATTTTGAATAGCAACCAACCA 828

Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	557	ACCAAGTGGTGAATTTACCAATCTTTGAATTTGATGTCGCCAAAGTGCAGTGCATGTC	616
Db	117	ACAGTGGTGAATTTACCAATCTTTGAATTTGATGTCGCCAAAGTGCAGTGCATGTC	176
QY	617	TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	676
Db	177	TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	236
QY	677	CAGCATTTGCTGAGCTGGTGTTCACAGAGCCTTCCAGTGAACATCATGATGCCTACCA	736
Db	237	CAGCATTTGCTGAGCTGGTGTTCACAGAGCCTTCCAGTGAACATCATGATGCCTACCA	296
QY	737	GGATCCGCGCTTTGATGAGAGGAGACAGATATCTGTTTTCACATAAAGATCTGTTCT	796
Db	297	GGATCCGCGCTTTGATGAGAGGAGACAGATATCTGTTTTCACATAAAGATCTGTTCT	356
QY	797	TTGTGTCCTTATTTGGAATAGCAACACCAATAATTTGAGTGGCTCAAGTGTAAACAG	856
Db	357	TTGTGTCCTTATTTGGAATAGCAACACCAATAATTTGAGTGGCTCAAGTGTAAACAG	416
QY	857	ACTTGATGGGAACCTTTTGATGATGAGATCAAGACTTTTGGGCTTTTGTGATCTT	916
Db	417	ACTTGATGGGAACCTTTTGATGATGAGATCAAGACTTTTGGGCTTTTGTGATCTT	476
QY	917	TTGTGGACTTGGCATCAACACAAATTTATGATCAAGTGAAGAAGTCTCTGGGCCAA	976
Db	477	TTGTGGACTTGGCATCAACACAAATTTATGATCAAGTGAAGAAGTCTCTGGGCCAA	536
QY	977	GCAGTCTGTGGCTTTGATGCTATCATACCATCAACATGTTCAAAAGCTGAAGTTGA	1036
Db	537	GCAGTCTGTGGCTTTGATGCTATCATACCATCAACATGTTCAAAAGCTGAAGTTGA	596
QY	1037	CAAGTTTAAAGCAGCAACATCCCTCTGGTGCAGAACTTGGCATCGATCATCTT	1096
Db	597	CAAGTTTAAAGCAGCAACATCCCTCTGGTGCAGAACTTGGCATCGATCATCTT	656
QY	1097	TGATGACTTTTCTCTGAGCTTTGATGCCATGATCACAGCTCTCTCCGGATGTTTCATGA	1156
Db	657	TGATGACTTTTCTCTGAGCTTTGATGCCATGATCACAGCTCTCTCCGGATGTTTCATGA	716
QY	1157	GCTGGGATGTGACAGAAATTTAAATTTGACTATGAGACATGTGTAGTGGCTTTTGAC	1216
Db	717	GCTGGGATGTGACAGAAATTTAAATTTGACTATGAGACATGTGTAGTGGCTTTTGAC	776
QY	1217	AGTGAGAAACTATCGATGGTCTTATACCAACCTGGAGACATGCTTCAACGTGTG	1276
Db	777	AGTGAGAAACTATCGATGGTCTTATACCAACCTGGAGACATGCTTCAACGTGTG	836
QY	1277	TCAGCTGATGTCGGGATGTTAAACACCTGCTGGGTTTCAAGACATTTGACCGAGGTGA	1336
Db	837	TCAGCTGATGTCGGGATGTTAAACACCTGCTGGGTTTCAAGACATTTGACCGAGGTGA	896
QY	1337	AAATTTAGGGTGTGTTGGGATGCTGTGATGACCTCGACACAGGGGAACCAACAA	1396
Db	897	AAATTTAGGGTGTGTTGGGATGCTGTGATGACCTCGACACAGGGGAACCAACAA	956
QY	1397	TGCTTCCAGCTAGAGTGGCTTGGCCCTGGCCCACTCTATGGAACCTCTGCTACCTT	1456
Db	957	TGCTTCCAGCTAGAGTGGCTTGGCCCTGGCCCACTCTATGGAACCTCTGCTACCTT	1016
QY	1457	GGAGCATCACCATTTCACACCAAGCTGATGATCTTCAAAAGTGGGTCACATATCTT	1516
Db	1017	GGAGCATCACCATTTCACACCAAGCTGATGATCTTCAAAAGTGGGTCACATATCTT	1076
QY	1517	TGCTAACCTGCTCCCAAGGAATATAGTGAACCTTATGACGCTTTTGAAGCAGTCAATAT	1576
Db	1077	TGCTAACCTGCTCCCAAGGAATATAGTGAACCTTATGACGCTTTTGAAGCAGTCAATAT	1136
QY	1577	GGCAACACCTCAGCTGTACTTTGAGAGAGAACTGAATTTCTTGAACCTTGCAGTAA	1636

Db	1137	GGCAACAGACCTCAGCGTGTACTTTGAGAGAGAACTGAATCTTTGAACCTTGCAGTAA	1196
QY	1637	AGGAGATACCATTTGGAAACATCAAAACCATCGTGATATATTTCGATCAATGTTAATGAC	1696
Db	1197	AGGAGATACCATTTGGAAACATCAAAACCATCGTGATATATTTCGATCAATGTTAATGAC	1256
QY	1697	AGCCTGTGACCTTTGGAGCCGTGACCAAAACCGTGGGAGATCTCCAGACAGTGGCAGAACT	1756
Db	1257	AGCCTGTGACCTTTGGAGCCGTGACCAAAACCGTGGGAGATCTCCAGACAGTGGCAGAACT	1316
QY	1757	TGTAAACAGTGTGATCTTCGAAACAGGAGATCGGGAGAGATTTAGAGCTCAAACTCACTCC	1816
Db	1317	TGTAAACAGTGTGATCTTCGAAACAGGAGATCGGGAGAGATTTAGAGCTCAAACTCACTCC	1376
QY	1817	TTCAGCAATTTTTCATGCGAACCGGAGGATGAATGCTCGTGGTTCGAACTGGAGTGGAT	1876
Db	1377	TTCAGCAATTTTTCATGCGAACCGGAGGATGAATGCTCGTGGTTCGAACTGGAGTGGAT	1436
QY	1877	TGATAGCATCTGTCATGCTTTTGTATCAGGCACTGGTGAAGCTCAACGTGAAACTGAAGCC	1936
Db	1437	TGATAGCATCTGTCATGCTTTTGTATCAGGCACTGGTGAAGCTCAACGTGAAACTGAAGCC	1496
QY	1937	GATGCTAGATTCAGTAGCTACAAACAGAACTAAGTGGGAGAGCTACACCAAAACGACT	1996
Db	1497	GATGCTAGATTCAGTAGCTACAAACAGAACTAAGTGGGAGAGCTACACCAAAACGACT	1556
QY	1997	GCTGGCTCAACTGCTCCTCCTCCTGCGAGTGTATGCTAGCAAGGAGACAG	2056
Db	1557	GCTGGCTCAACTGCTCCTCCTCCTGCGAGTGTATGCTAGCAAGGAGACAG	1616
QY	2057	GAACATA 2063	
Db	1617	GAACATA 1623	
RESULT 8			
ID	AAH78223	standard; DNA; 2513 BP.	
XX	AAH78223;		
AC	AAH78223;		
XX	26-NOV-2001	(first entry)	
DT	Nucleotide sequence of a human phosphodiesterase polypeptide.		
XX	Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;		
DE	nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;		
KW	osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;		
KW	Parkinson's disease; dementia; infectious disease; malignant tumour; ss.		
XX	Homo sapiens.		
OS	Key		
XX	Location/Qualifiers		
EH	1..1425		
FT	/*tag= a		
FT	/product= "phosphodiesterase"		
XX	WO200166716-A1.		
PN	13-SEP-2001.		
PD	06-MAR-2001; 2001WO-JP01720.		
XX	07-MAR-2000; 2000JP-0061464.		
PR	10-JUL-2000; 2000JP-0208610.		
XX	(KYOW) KYOWA HAKKO KOGYO KK.		
PA	Miyaaji H, Haruoka M, Ota T, Kawabata A, Sugano S, Nakamura Y;		
XX	WPI: 2001-570769/64.		
PI	P-PSDB; AAG67531.		
DR			
XX			

PT Polypeptides with phosphodiesterase activity and DNA for treatment of
PT diabetes, ischemic heart disease, hypertension, nephritis,
PS pancreatitis, ulcers, allergies, asthma
XX Claim 3; Page 82-86; 105pp; Japanese.

CC The present sequence encodes a human polypeptide which has
CC phosphodiesterase activity. The phosphodiesterase polypeptide and
CC polynucleotide are used for the treatment and prevention of diabetes,
CC ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers,
CC allergies, asthma, rheumatism, osteoporosis, pain, anxiety,
CC schizophrenia, manic depressive psychosis, Parkinson's disease,
CC dementia, infectious diseases, and malignant tumours.

XX Sequence 2513 BP; 761 A; 528 C; 565 G; 659 T; 0 other;

Query Match	68.4%;	Score 1421.8;	DB 22;	Length 2513;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1423;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 639	ATGGAGAATCATCATCTCCGACTGGCTAATAATAACAGCATTCGCTGAGCTGGTTGCT	698		
DB 1	ATGGAGAATCATCATCTCCGACTGGCTAATAATAACAGCATTCGCTGAGCTGGTTGCT	60		
QY 699	TCAACAGCCCTCCAGTGAACATCAGTGCCTACAGGATCCGCGCTTTGATGCAGAG	758		
DB 61	TCAACAGCCCTCCAGTGAACATCAGTGCCTACAGGATCCGCGCTTTGATGCAGAG	120		
QY 759	CGACACAGATCTGTTTTCACATAAGATCTGTTCTTGTGTCCTTATTGGATAGC	818		
DB 121	CGACACAGATCTGTTTTCACATAAGATCTGTTCTTGTGTCCTTATTGGATAGC	180		
QY 819	AACCACCAATTAATGGAGTGGCTCAAGTGTAAACAGACTTGTGGAAACCTTTTGAT	878		
DB 181	AACCACCAATTAATGGAGTGGCTCAAGTGTAAACAGACTTGTGGAAACCTTTTGAT	240		
QY 879	GATGCAGATCAACGACTTTTGGAGCTTTTGTATCTTTTGTGACTTTGGCATCAACAC	938		
DB 241	GATGCAGATCAACGACTTTTGGAGCTTTTGTATCTTTTGTGACTTTGGCATCAACAC	300		
QY 939	ACAATTATGATGATCAAGTGAAGAGTCTGGGCAAGCAGTCTGTGGCTCTTGATGTG	998		
DB 301	ACAATTATGATGATCAAGTGAAGAGTCTGGGCAAGCAGTCTGTGGCTCTTGATGTG	360		
QY 999	CTATCATACCATGCAACATGTTTCAAAAGCTGAAGTTGACAACTTTAAGCAGCCCAACATC	1058		
DB 361	CTATCATACCATGCAACATGTTTCAAAAGCTGAAGTTGACAACTTTAAGCAGCCCAACATC	420		
QY 1059	CCTCTGGTGTGAGAACTTGGCCATGATGACATTCATTTTGTATGACTTTTCTCTCGACGTT	1118		
DB 421	CCTCTGGTGTGAGAACTTGGCCATGATGACATTCATTTTGTATGACTTTTCTCTCGACGTT	480		
QY 1119	GATGCCATGATCAGACGCTCTCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTT	1178		
DB 481	GATGCCATGATCAGACGCTCTCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTT	540		
QY 1179	AAATTTGACTATGAGACACTGTGTAGTGGCTTTTTCACAGTGAAGAAACCTATCGGATG	1238		
DB 541	AAATTTGACTATGAGACACTGTGTAGTGGCTTTTTCACAGTGAAGAAACCTATCGGATG	600		
QY 1239	GTTCTATACCACTGGAGACATGCCCTTCAACGTGTGTGATGCTGTGCGCATGTTA	1298		
DB 601	GTTCTATACCACTGGAGACATGCCCTTCAACGTGTGTGATGCTGTGCGCATGTTA	660		
QY 1299	ACCACTGCTGGTTCACAGACATTCCTACCGAGTGGAAATTTTAGCGGTGATTTGGGA	1358		
DB 661	ACCACTGCTGGTTCACAGACATTCCTACCGAGTGGAAATTTTAGCGGTGATTTGGGA	720		
QY 1359	TGCTGTGTGATGACCTCGACACAGGGGAACCAACATGCTTCCAAGCTAAGAGTGGC	1418		
DB 721	TGCTGTGTGATGACCTCGACACAGGGGAACCAACATGCTTCCAAGCTAAGAGTGGC	780		
QY 1419	TCGTCCCTGGGCCAACTCTATGGAACCTCTGTACCTTTGGAGCATCACCATTTCACAC	1478		

DB 781	TCTGCCCTGGCCCAACTCTATGGAACTCTGTACCTTTGGAGCATCACCATTTCACAC	840		
QY 1479	GCCGTGATGATCTTCAAGTGAGGTCACAAATATCTTTGCTTAACCTCTCTCCCAAGGAA	1538		
DB 841	GCCGTGATGATCTTCAAGTGAGGTCACAAATATCTTTGCTTAACCTCTCTCCCAAGGAA	900		
QY 1539	TATAGTAGCTTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACTCACGCTGTAC	1598		
DB 901	TATAGTAGCTTATGACAGCTTTTGAAGCAGTCAATATTTGGCAACAGACTCACGCTGTAC	960		
QY 1599	TTTGAGAGGAGAACTGAATCTTTGAACTTGTGCTAAGGAGATAGATTGGAAATC	1658		
DB 961	TTTGAGAGGAGAACTGAATCTTTGAACTTGTGCTAAGGAGATAGATTGGAAATC	1020		
QY 1659	AAAAACCATCTGTATATATTTTCGATCAATGTTAATGACAGCTGTGACCTTTGGAGCCGTG	1718		
DB 1021	AAAAACCATCTGTGTATATTTTCGATCAATGTTAATGACAGCTGTGACCTTTGGAGCCGTG	1080		
QY 1719	ACCAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTTGTAACAGTGAAGTTCTTCGAA	1778		
DB 1081	ACCAACCGTGGGAGATCTCCAGACAGGTGGCAGAACTTTGTAACAGTGAAGTTCTTCGAA	1140		
QY 1779	CAAGGAGATCGGGAGAGATTAGAGCTCAAACTCACTCCTTCAGCAATTTTGTGATCGGAAC	1838		
DB 1141	CAAGGAGATCGGGAGAGATTAGAGCTCAAACTCACTCCTTCAGCAATTTTGTGATCGGAAC	1200		
QY 1839	CGGAAGGATGAACCTCCCTCGGTGGTCACTGGAGTGGATTGATAGCATCTGCATGCTTTG	1898		
DB 1201	CGGAAGGATGAACCTCCCTCGGTGGTCACTGGAGTGGATTGATAGCATCTGCATGCTTTG	1260		
QY 1899	TATCAGGCACTGGTGAAGTCAACGTGAAGCTGAAGCCGATGCTAGATTTCAGTAGTACA	1958		
DB 1261	TATCAGGCACTGGTGAAGTCAACGTGAAGCTGAAGCCGATGCTAGATTTCAGTAGTACA	1320		
QY 1959	AACAGAACTAGTGGGAAGAGCTACCAAAACAGCTGCTGGCTCAACTGCCCTCATGCC	2018		
DB 1321	AACAGAACTAGTGGGAAGAGCTACCAAAACAGCTGCTGGCTCAACTGCCCTCATGCC	1380		
QY 2019	TCCTCCCTGCCAGTGTATGTCACCAAGGAAGACAGAACTAA	2063		
DB 1381	TCCTCCCTGCCAGTGTATGTCACCAAGGAAGACAGAACTAA	1425		
RESULT 9	AAA49973			
ID	AAA49973 standard; cDNA; 1982 BP.			
XX	AAA49973;			
XX	10-OCT-2000 (first entry)			
DE	Human cyclic nucleotide phosphodiesterase HSPDE10A2 cDNA.			
KW	Cyclic nucleotide phosphodiesterase; HSPDE10A2; human; cancer;			
OS	immune disorder; diagnosis; therapy; ss.			
XX	Homo sapiens.			
FT	Key	Location/Qualifiers		
XX	CDS	157..1260		
XX		/*tag= a		
PN	WO200040733-A1.			
PD	13-JUL-2000.			
PF	07-JAN-2000; 2000WO-US00371.			
PR	07-JAN-1999; 99US-0226741.			
PA	(INCY-) INCYTE PHARM INC.			
XX				

PI Phillips SC, Lanfear J, Fawcett L, Bandman O, Harrow I;
 XX WPI: 2000-452539/39.
 DR P-PSDB; AAY95522.
 XX New human cyclic nucleotide phosphodiesterases, referred as HSPDE10A1
 PT and HSPDE10A2, useful for treating and preventing cancer and immune
 PT disorders -
 PT
 XX Claim 4; Page 85-86; 96pp; English.
 PS
 XX The present sequence is that of cDNA encoding HSPDE10A2 (see
 CC AAY95522), a novel human cyclic nucleotide phosphodiesterase. The
 CC cDNA was initially identified in Incyte Clone 826776 from the
 CC prostate cDNA library PROSTUT04 using BLAST analysis and human
 CC phosphodiesterase 5 as query. Full-length cDNA sequences of
 CC HSPDE10A2 were obtained from a human skeletal muscle library using
 CC the complete cDNA insert of Incyte Clone 826776 as probe.
 CC HSPDE10A2 is a C-terminal splice variant of HSPDE10A1 (see AAY95521).
 CC The invention provides expression vectors, host cells, antibodies,
 CC agonists and antagonists, as well as methods for diagnosing,
 CC treating or preventing disorders associated with expression of
 CC HSPDE10A, especially cancer and immune disorders. A fragment of
 CC the present sequence from about nucleotide 1183 to nucleotide 1227
 CC is useful in hybridisation or amplification technologies to
 CC distinguish HSPDE10A2 sequences from related sequences.
 XX
 SQ Sequence 1982 BP; 592 A; 421 C; 425 G; 544 T; 0 other;

Query Match 50.3%; Score 1045.6; DB 21; Length 1982;
 Best Local Similarity 99.6%; Pred. No. 1.1e-314;
 Matches 1048; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 557 ACCAGTGTGAAATTTACCAATCTTGAATTTGATGTCCTCCCAAGTCGATGTC 616
 DB 123 ACAGGTGTGAAATTTACCAATCTTGAATTTGATGTCCTCCCAAGTCGATGTC 182
 QY 617 TGAGAACAGTTTCAAGAACGATGGAGAAATCATCATCTCCGACTGGCTAAATAA 676
 DB 183 TGAGAACAGTTTCAAGAACGATGGAGAAATCATCATCTCCGACTGGCTAAATAA 242
 QY 677 CAGCATTCCTGAGCTGGTGTTCACAGGCTTCACGATGATGATGATGATGATG 736
 DB 243 CAGCATTCCTGAGCTGGTGTTCACAGGCTTCACGATGATGATGATGATGATG 302
 QY 737 GGATCCGCGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 796
 DB 303 GGATCCGCGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 362
 QY 797 TTGCTCCCTATTTGGAATAGCAACCAACCAATATTTGAGTGGCTCAAGTGTAAACAG 856
 DB 363 TTGCTCCCTATTTGGAATAGCAACCAACCAATATTTGAGTGGCTCAAGTGTAAACAG 422
 QY 857 ACTTGATGGGAACCTTTTGATGATGATGATGATGATGATGATGATGATGATGAT 916
 DB 423 ACTTGATGGGAACCTTTTGATGATGATGATGATGATGATGATGATGATGATGAT 482
 QY 917 TTGCTGACTTGGCATCAACACACAAATATGATGATGATGATGATGATGATGATGAT 976
 DB 483 TTGCTGACTTGGCATCAACACACAAATATGATGATGATGATGATGATGATGATGAT 542
 QY 977 GCAGTCTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1036
 DB 543 GCAGTCTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 602
 QY 1037 CAAGTTTAAAGCAGCCACATCCCTCTGGTGTGATGATGATGATGATGATGATGAT 1096
 DB 603 CAAGTTTAAAGCAGCCACATCCCTCTGGTGTGATGATGATGATGATGATGATGAT 662
 QY 1097 TGATGACTTTTCTCGAGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 1156
 DB 663 TGATGACTTTTCTCGAGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 722

QY 1157 GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 1216
 DB 723 GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 782
 QY 1217 AGTGAGGAAAACTATCGGATGGTGTCTATACCACTGGAGACATGCTTCAACGTGTG 1276
 DB 783 AGTGAGGAAAACTATCGGATGGTGTCTATACCACTGGAGACATGCTTCAACGTGTG 842
 QY 1277 TCAGCTGATGTCGGGATGTTAAACCACTGCTGGGTTCAGACATTCGACCGAGGTGA 1336
 DB 843 TCAGCTGATGTCGGGATGTTAAACCACTGCTGGGTTCAGACATTCGACCGAGGTGA 902
 QY 1337 AATTTACGGGTGATTTGGGATGCTGTGTCATGACCTCGACACAGGGGAACCAAA 1396
 DB 903 AATTTACGGGTGATTTGGGATGCTGTGTCATGACCTCGACACAGGGGAACCAAA 962
 QY 1397 TGCTTCCAAAGCTAAGAGTGGCTGTGCTGCTGGCCCAACTCTATGAAACCTCTGCTACCTT 1456
 DB 963 TGCTTCCAAAGCTAAGAGTGGCTGTGCTGCTGGCCCAACTCTATGAAACCTCTGCTACCTT 1022
 QY 1457 GGAGCATCACCATTTCACACCGCGCTGATGATCCTTCAAAAGTGAAGGTCACAATATCTT 1516
 DB 1023 GGAGCATCACCATTTCACACCGCGCTGATGATCCTTCAAAAGTGAAGGTCACAATATCTT 1082
 QY 1517 TGCTAACCTGTCTCCCAAGGAATATAGTACCTTATGACGCTTTTGAAGCAGTCAATATT 1576
 DB 1083 TGCTAACCTGTCTCCCAAGGAATATAGTACCTTATGACGCTTTTGAAGCAGTCAATATT 1142
 QY 1577 GGCAACAGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1608
 DB 1143 GGCAACAGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1174

RESULT 10
 AAD28571
 ID AAD28571 standard; cDNA; 426 BP.
 XX
 AC AAD28571;
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PDE-like enzyme encoding cDNA #2.
 XX
 KW Human; phosphodiesterase; PDE-like enzyme; benign prostate hyperplasia;
 KW urinary incontinence; erectile dysfunction; cardiovascular disorder;
 KW cancer; diabetes; ischaemic disease; myocardial infarction; cytostatic;
 KW vasodilator; cardiant; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..426
 FT /*tag= a
 FT /product= "Human PDE-like protein"
 FT /note= "CDS does not include start and stop codon"
 FT /partial
 XX
 PN WO200200854-A2.
 XX
 PD 03-JAN-2002.
 XX
 XX 26-JUN-2001; 2001WO-EP07289.
 XX
 XX 26-JUN-2000; 2000US-213998P.
 PR 25-MAY-2001; 2001US-293221P.
 XX
 XX (FARB) BAYER AG.
 XX
 XX Ramakrishnan S;
 PI
 XX WPI: 2002-090522/12.
 DR P-PSDB; AAD28571.
 XX

Isolated polynucleotide encoding a human phosphodiesterase-like enzyme, useful for treating a disease such as urinary incontinence, benign prostate hyperplasia, erectile dysfunction, diabetes, cancer or cardiovascular disorder -

Claim 1b; Fig 4; 165pp; English.

The present invention relates to human phosphodiesterase (PDE)-like enzymes and their corresponding polynucleotides. The invention also relates to reagents which regulate PDE-like enzyme activity and reagents which bind to human PDE-like enzyme gene products which can be used to regulate degradation of cGMP. Sequences of the invention are useful for modulating the activity of a PDE-like enzyme in a disease such as urinary incontinence, benign prostate hyperplasia, erectile dysfunction, cancer, diabetes or cardiovascular disorder (e.g. ischemic diseases, myocardial infarction). The present sequence is a cDNA encoding human PDE-like enzyme.

Sequence 426 BP; 137 A; 76 C; 94 G; 119 T; 0 other;

Query Match 18.7%; Score 388.8; DB 24; Length 426;
Best Local Similarity 99.5%; Pred. No. 2.3e-110;
Matches 390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

171 GATGACGATCAATGATGAATCGAAGCTGACTGGATACAGACAAAATCAATTATG 230
1 GATCGACGATTCATGATGAATCGAAGCTAAGCTAAGTGGATACAGACAAAATCAATTATG 60
231 TGCATGCCATCCGAGCAGTGATGGTCAGATTTATTTGGTGGCCCAAGCGGATAAAG 290
61 TGCAFGCCATCCGAGCAGTGATGGTCAGATTTATTTGGTGGCCCAAGCGGATAAAG 120
291 ATTCTCTGAAGAGTCCATTTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTCCA 350
121 ATTCTGAAGAGTCCATTTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTTCCA 180
351 TTTTGTGGAATCGGCATATCAAGCTCAGCTCTTTTGTGCTCAAGGAAAGAAATATGAA 410
181 TTTTGTGGAATCGGCATATCAAGCTCAGCTCTTTTGTGCTCAAGGAAAGAAATATGAA 240
411 AGAGCAGAGCTTTGCTAGAGTGGTTAATGACCTCTTTGAAGACACACTGACCTGGAG 470
241 AGAGCAGAGCTTTGCTAGAGTGGTTAATGACCTCTTTGAAGACACACTGACCTGGAG 300
471 AAAATTGTCAAGAAATATGATCGCGGCCCAAACTCTGCTGAAATGTGAGCGCTGTTCT 530
301 AAAATTGTCAAGAAATATGATCGCGGCCCAAACTCTGCTGAAATGTGAGCGCTGTTCT 360
531 GTTTTACTCTAGAGGACATCGAATCACCAGT 562
361 GTTTTACTCTAGAGGACATCGAATCACCAGT 392

RESULT 11

AAA39042
ID AAA39042 standard; cDNA; 2499 BP.

AC
XX

AA39042;

25-AUG-2000 (first entry)

Human cGMP phosphodiesterase V encoding cDNA SEQ ID NO:2.

Human; cGMP phosphodiesterase V; inhibitor; tricyclic compound;
cyclic GMP phosphodiesterase inhibitor; erectile failure;
feminine function failure; ds.

Homo sapiens.

JP2000095759-A.

04-APR-2000.

XX

PF 19-JUL-1999; 99JP-0204103.

XX 21-JUL-1998; 98JP-0204963.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 2000-353412/31.

DR P-PSDB; AAY90912.

XX Tricyclic compounds having cyclic GMP-specific phosphodiesterase

PT inhibitory action useful as pharmaceuticals, and preparation and agents

PT thereof -

XX Example 117; Page 68-69; 71pp; Japanese.

PS The present invention describes cyclic GMP (cGMP)-specific

CC phosphodiesterase inhibitors comprising tricyclic compounds or their

CC salts. The inhibitors are useful for the treatment and prevention of

CC erectile failure and feminine function failure. The compounds have

CC excellent cGMP-phosphodiesterase inhibitory action. The present

CC sequence encodes human cGMP phosphodiesterase V, which is used in an

CC example from the present invention.

XX Sequence 2499 BP; 778 A; 493 C; 563 G; 565 T; 0 other;

SQ Query Match 17.2%; Score 356.6; DB 21; Length 2499;

Best Local Similarity 52.0%; Pred. No. 7.7e-100;

Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;

QY 159 AGGATCGACGATTCATGATGAATCGACACAGCTGACTGGATACAGACAAAATCAATTTAT 228

Db 614 AGGATCTCTCGTTCATGAGAGTTGACCAAAATTTACAGGCTACAGACACAAAAGCATTC 673

QY 229 TGTGATCCCTATCCGAAGCAGTGATGCTGAGATTTATTTGGTGGCCCAAGCGATAAATA 288

Db 674 TTTGATGCCAATTAAGAATCATAGGAAGAGTTGTTGGTGGCCCAAGCGCCATCAACA 733

QY 289 AGATTCTCTG---AAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATC 345

Db 734 AGAATCAGGAAACGCTGGACATTTACTGAAAGAGATGAAAGGACTTTGTGCTTAT 793

QY 346 TTCCATTTTGGAAATCGGCATATCTAAGCTCAGCTCTTTGCTGCCCAAGGAAAGAT 405

Db 794 TGGCATTTTGGTATTTCTTCATAATGCTCAGCTCTATGAGACTTCTCAGCTGGAGA 853

QY 406 ATGAAAGAGCAGAGCTTTTGTAGAGTGGTTTATGACCTCTTTCAAGAACAGACTGACC 465

Db 854 ACAAGAGAAATCAGTGCTGCTTGACCTTGTAGTTTAAATTTTGAAGAACACAAATCAT 913

QY 466 TGGAGAAAATTTCAAGAAAATTAATGTCATCGGGGCCCAAACTCTGCTGAAATGTGACGCT 525

Db 914 TAGAAGTAATTTTGAAGAAAATAGCTGCCACTTATTTCTTTCATGCAAGTGCAGAAAT 973

QY 526 GTTCTGTTTTTACTCTAGAGGACATCGAATCACCAGTGGTGAATTTTACCAATCCTTTG 585

Db 974 GCACCAATTTTCATAGTGGATGAAGATTGCTCCGATTTCTTTTCTAGTGTGTTACATGG 1033

QY 586 AATTGATGTCCCAAGTGCAGTGTGCTGATGCTGAGAACAGTTTCAAGAAAGACGGAGA 645

Db 1034 AGTGTGAGGAATTAGAAAAATCATCTGATACATTAACAGGGAACATGATGCAACAAAA 1093

QY 646 AATCATCATCTCCGACTGGCTTAATAAATACAGCATTTGCTGAGTGGTTGCTTCAACAG 705

Db 1094 TCAATTACATGTATGCTCAGTATGCAAAAAATACATGGAACCACTTAATATCCAGATG 1153

QY 706 GCTTCCAGTGAACATCAGT-----GATGCTCACCAGGATCCGCCCTTTGATGACAGAGC 760

Db 1154 TCAGTAAGGATAAAAGATTTCCCTGGACAAATTAACAGAAATGTAACACAGCAGT 1213

QY 761 AGACCAGATATCTGTTTTTCATCAATGAATCTGTTCTTTTGTGCTCCCTATTTTGAATAGCAA 820

Db 1214 GCATTAGAAGTTTGTCTTTGTACACCTTATAAAAAATGGAAAGAAAGTAAGTTATAGGGG 1273

Db 794 TGGCATTTTGGGTATTTGTTCTTCAATATGCTAGCTCTATGAGACTTCACTGCTGGAGA 853
Qy 406 ATGAAGAAGACAGAGCTTTTGTAGAGTGGTTAATGACCTCTTTTGAAGAACAGACTGACC 465
Db 854 ACAAGAGAATACAGTGTCTTACCTTGTGCTAGTTTAAATTTTGAAGAACAAACAATCAT 913
Qy 466 TGGAGAAAATTTGTCAGAAAATATATGATCGGGGCCCAAACTCTGCTGAAATGTCAGCGCT 525
Db 914 TAGAAGTAAATTTTGAAGAAAATAGCTGCCACTATTATCTCTTTCATGCAAGTCAGAAAT 973
Qy 526 GTTCTGTTTACTCTAGAGGACATCGAATCAACAGCTGGTGAATTTTACCAAAATCCTTTTG 585
Db 974 GCACCATTTTCATAGTGGATGAAGATTTGCTCCGATTTCTTTTCTAGTGTGTTTTCACATGG 1033
Qy 586 AATTGATGTCTCCCAAGTGCAGTCTGATGCTGAGAACAGTTTCAAGAAAAGCATGGAGA 645
Db 1034 AGTGTGAGGAATTAGAAAAATCATCTGATACATTAAACAAGGGAACATGATCAACAACAA 1093
Qy 646 AATCATCATCTCCGACTGGCTAATAATACAGCATTTGCTGAGCTGGTTCCTTCAACAG 705
Db 1094 TCAATTACATGTATGCTCAGTATGTCAAAAATACATATGGAACCACTTAAATATCCAGATG 1153
Qy 706 GCCTTCCAGTCAACATCAGT-----GATGCCCTACCAGGATCCGCTTTGATGCGAGGC 760
Db 1154 TCAGTAGGATAAAGATTTCCCTGGCAACTGAAATACAGAAATGTAACACGAGT 1213
Qy 761 AGACCAGATATCTGGTTTTCATATAAGATCTGTTTGTGTCTCCTATTTTGAATAGCAA 820
Db 1214 GCATTAGAAGTTTCTTGTACACTATAAAAATGGAAGAAGAAATTAAGTTATAGGG 1273
Qy 821 CCACCAATAATTTGGAGTGGCTCAAGTGTAAACAGACTTGTATGGGAACCTTTTGATGA 880
Db 1274 TTTGCCAACTTGTAAATAAGATGGAGGAGAAATACTGGC--AAGGTTAAGCCTTTCAACCG 1331
Qy 881 TGCAGATCAACGACTTTTGGAGCTTTTGTTCATCTTTGTGAGCTTGCATCAACAACAC 940
Db 1332 AATGACGAACAGTTTCTGGAAGCTTTTGTTCATCTTTTGTGCTTGGGATCCAGAACAC 1391
Qy 941 AATTATGATGATCAAGTGAAGAAGTCTGGGCCCAAGCAGTCTGTGGCTCTTGATGTCT 1000
Db 1392 GCAGATGATGAAGCAGTGGAGAGAGCCATGCCCAAGCAATGTTCACATTTGGAGTTCT 1451
Qy 1001 ATCATACCATGCACATGTTTCAAAGCTGAAGTTGACAAAGTTTAAGGAGCCACATCC 1060
Db 1452 GTCGTATCATCTTCAGCAGCAGAGGAGAAACAAGAGAGCTACAGTCTTTAGCGGCTGC 1511
Qy 1061 TCTGGTGTC-----GAACCTTGCATCGATGACATTCATTTTGATGACTTTTCTCT 1111
Db 1512 TGTGGTGCCTCTGCCAGACCCCTTAAATTTACTGACTTTTACGCTTACGTTGAGCT 1571
Qy 1112 CGAGCTTGTATGCCATGATACAGCTGCTCTCCGGATGTTTCAAGCTGGGGATGGTACA 1171
Db 1572 GTCTGATCTGGAACAGCAGCTGTGTACAATTCGGATGTTTACTGACCTCAACCTTGTGCA 1631
Qy 1172 GAAATTTAAATTTGACTATGACATGACACATGCTGTAGTGGCTTTTGACAGTGAGAAAAC 1231
Db 1632 GAACCTTCAGATGAACATAGAGTTCTTTTGAGATGGATTTTAAAGTGTAAAGAAATTA 1691
Qy 1232 TCGGATG---GTTCTATACCACTTGGAGACATGCTTCAACGTTGCTGAGCTGATGTT 1288
Db 1692 TCGAGNAGATGTTGCCCTATCATATTTGGAGACATGCCCTTTAATACAGCTAGTGCATGT 1751
Qy 1289 CGCGATGTTAACCACTGCTGGGTTTCAAGACATTTCTGACCGAGGTGGAAATTTTAGCGGT 1348
Db 1752 TGCTGCTCTAAAGCAGCAAAATTCAGAACAAAGCTGACTGAACCTGGAGATACITGCATT 1811
Qy 1349 CATTGTGGGATGCTGCTGCTATGACTCGACCCAGAGGGGAACCAACATGCTTCCAAAGC 1408
Db 1812 GCTGATTTGCTGCATCAAGCCACAGATTTGGATCAACCGTGTGTGAATACTCTTACATACA 1871
Qy 1409 TAAGAGTGGCTTGCCTTGGCCCACTCTATGGAACCTCTGCTACCTTGGAGACATCACCA 1468
Db 1872 CGAAGTGAACATCCACTTGGCCAGCTTTTACTG---CCATTCAATCATGGAACACCATCA 1928

RESULT 13
AAF99963

ID AAF99963 standard; cDNA; 2499 BP.

XX AAF99963;

XX 16-JUL-2001 (first entry)

XX Human phosphodiesterase-V cDNA.

XX Human; phosphodiesterase-V; PDE-V; antianginal; cardiant; hypotensive;
antiarteriosclerotic; antiallergic; antiasthmatic; nephrotropic;
immunostimulant; ophthalmological; vasotropic; pyrimidine-5-carboxamide;
cGMP-specific PDE inhibitor; heart disorder; allergy; immunodeficiency;
eye disorder; fertility; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..2499

XX /*tag= a

XX /partial

XX /note= "this sequence does not contain a stop codon"

XX /product= "PDE-V"

XX WO200127105-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-JP07048.

XX 12-OCT-1999; 99JP-0289868.

XX (TAKE) TAKEDA CHEM IND LTD.

XX

PI	Miwa T, Yamamoto M, Doi T, Tarui N;
XX	
XX	WPI: 2001-273753/28.
XX	P-PSDB: AAB97024.
XX	
XX	New pyrimidine-5-carboxamide compounds are cGMP-specific
PT	phosphodiesterase inhibitors for treating e.g. angina pectoris,
PT	allergies and immunodeficiencies -
XX	
XX	Example 3; Page 333-334; 241pp; Japanese.
XX	
XX	The present sequence encodes human phosphodiesterase-V (PDE-V). The
CC	invention relates to novel pyrimidine-5-carboxamide compounds which may
CC	be used as cGMP-specific phosphodiesterase (cGMP-PDE) inhibitors,
CC	especially cGMP-specific phosphodiesterase-V (cGMP-PDE-V) inhibitors.
CC	cGMP-PDE-V inhibitors are useful for treating and preventing angina
CC	pectoris, cardiac insufficiency, myocardial ischaemia, hypertension,
CC	pulmonary hypertension, arteriosclerosis, allergic disorders, asthma,
CC	neuropathies, cerebral fibrosis, immunodeficiency, eye disorders and
CC	male or female sexual dysfunction.
XX	
SQ	Sequence 2499 BP: 778 A; 493 C; 563 G; 665 T; 0 other:

Query Match	17.2%	Score 356.6	DB 22	Length 2499
Best Local Similarity	52.0%	Pred. No. 7.7e-100		
Matches 954	Conservative 0	Mismatches 854	Indels 25	Gaps 6
QY	169	AGGATCGACGATTC	AAATGATGAATCACAAGCTGACTGGATACAAAGCAAAATCA	TAT 228
DB	614	AGATCCTCGTTCA	ATGCGAGAGTTGACCAATACAGGCTACAGACACAAGCAATC	673
QY	229	TGTGCATGCCAT	CCGAAGCAGTGATGGTGAGATATTGGTGTGGCCCAACGCGATAA	288
DB	674	TTTGTATGCCAAT	AAGAATCATAGGAAGAGGTTGTTGGTGTAGCCCGACGCCATCA	733
QY	289	AGATTCCG---	AAGGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATG	345
DB	734	AGAAATCAGAAAC	GGTGGGACATTTACTGAAAAGATGAAAAGGACTTTGCTGCTTAT	793
QY	346	TTCCATTTTGTG	GAATCGCCATATCTAACGCTCAGCTCTTTGCTGCCCTCAAGGAAAGA	405
DB	794	TGSCATTTTGCT	ATTTGTTCTTCATAATGCTCAGCTCTATGAGACTTCACTGCTGG	853
QY	406	ATCAAGAGACG	AGCTTTGCTAGAGTGTTTATGACCTCTTTGAAGACAGACTGACC	465
DB	854	ACAAGAGAAAT	CAGTGCTGCTTGACCTGCTAGTTTAATTTTGAAGAACAACAATCAT	913
QY	466	TGAGAGAAAT	TGTCAGAAAAATATGATCGGGCCCAACTCTGCTCAAAATGTGAGCGCT	525
DB	914	TAGAAGTAAT	TTTGAGAAAAATAGTGCACACTATTATCTCTTCATGCCAAGTGCAGAAAT	973
QY	526	GTTCTGTTTACT	CCCTAGAGGACATCGAATCACCAGTGGTGAATTTTACCAAAATCCTTTG	585
DB	974	GCACCATTTTCA	TAGTGGATGAAGATTGCTCCGATTCTTTTCTAGTGTGTTTCACATGG	1033
QY	586	AATTGATGCCCC	AAAGTCAGTGCTCATGCTGAGAACAGTTTCAAGAAGCATGAGAGA	645
DB	1034	AGTGTGAGGAAT	TAGAAAAATCATCTGATACATTAACAAAGGAACAATGATGCAAAACAAA	1093
QY	646	AATCATCATACT	CCGACTGGCTAATAAATACAGCATTGTGAGCTGGTTGCTTCAACAG	705
DB	1094	TCAATTACATG	TATGCTCAGTATGTCAAAATACTATGGAACCACTTAATATCCCAGATG	1153
QY	706	GCCTCCAGTGA	ACATCAGT-----GATGCCATACAGGATCCGGGCTTTGATCGAGAGC	760
DB	1154	TCAGTAAGGATA	AAAGATTTCCCTGGGACACTGAAAATACAGGAAATGTAACACGACGT	1213
QY	761	AGACCAGATATC	TGGTTTTCACATAAGATCTGTTCTTTGTGTCCTATTTTGGAATAGCAA	820
DB	1214	GCATTAGAAG	TTTGCTTTGTACACCTATAAAAATGGAAGAGAAATAAAGTTATAGGG	1273
QY	821	CCACCAAAAT	TAATTTGGAGTGGCTCAAGTGTATAACAGACTTGATGGGAAACCTTTTGATGA	880

1274	TTTGCCCAACTTGTTTATAAAGATGGAGGAGAAATACTGGC--AAGGTTAAGGCTTTTCAACCG	1333
881	TGCAGATCAACGACGCTTTTGGAGGCTTTTGTGTCATCTTTTGTGGACTTGGCATCAACAACAC	940
1332	AAATGACGAACAGTTTCTTGGAACTTTTGTCACTTTTGTGGCTTGGGATCCAGAACAC	1391
941	AATTATGATGATCAAGTAGAGTGAAGTCTCTGGGCCAAGCAGTCTGTGGCTTGTGATGTGCT	1000
1392	GCAGATGATGAAGCAGTGGAGAGAGCCATGGCCAGCAAAATGTCACATTTGAGAGTCTCT	1451
1001	ATCATACCATGCAACATGTCACAAAGCTGAAGTTTGACAGTTTAAAGCAGCCCAACATCCC	1060
1452	GTCGATATGCTTACAGACGAGGAGAAACAAGAGAGCTACTAGCTGTTAGCGCTGTC	1511
1061	TCGTGGTGTCA-----GAACTTGGCATCGGATGACATTCATTTTGTGACATTTTCTCT	1111
1512	TGTGGTGCCATCTGCCCAGACCCCTTAAATTAATCTGACTTTTACGTTTCAGTTCAGCT	1571
1112	CGAGTTTGATGCCATGATCATCAGCTGCTCTCCGGATGTTTCATGGAGCTGGGATGGTACA	1171
1572	GTCGTGATCTGGAACACGACACTGTGTACAAATTCGAGTGTTTTACTGACCTCAACCTTCGCA	1631
1172	GAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTTCAGACTGAGGAAAAACTA	1231
1632	GAATCTCCAGATGAACATCAGGTCTCTTTCGAGATGGATTTTAAGTGTTTAAGAAGAAATTA	1691
1232	TCGGATG---GTTCTATACCACAACTGGAGACATGCTTCAACGTGTGTGACGTGATGTT	1288
1692	TCGGAAGAATGTTGGCCTATCATTAATTTGGAGACATGCTTTTAATACAGCTCAGTGGCATGTT	1751
1289	CGGATGTTAAACCACTGCTGGGTTTCAAGACATCTTGACCGAGGTGGAAATTTAGCGGT	1348
1752	TGCTGCTCTAAAGCAGGCAAAATTCAGAACAGCTGACTGACCTGGAGATCTTCGATT	1811
1349	GATTTGGGATGCTGTGTGTCATGACCTCGACCACAGGGGAACCAACAATGCCCTTCCAAGC	1408
1812	GCTGATTTGCTGCACTAAGCCACGATTTGGATCACCGTGGTGTGAATAAATCTTTACATACA	1871
1409	TAAGATGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTACCTTGGAGCATCACCA	1468
1872	GCGAAGTGAACATCCACTTCCCGCAGCTTTACTG---CCATTAATCATGGAACACCATCA	1928
1469	TTTTCAACGCGCGTGATGATCTCTTCAAGTGAAGGTCAACAATATCTTTGCTAACCTGTG	1528
1929	TTTTGACCACTGCTGTATGATCTTAATAGTCCAGGCAATCAGATTTCTCAGTGGCCTCTC	1988
1529	CTCCAAGAAATATAGTGACCTTATGACGCTTTTGAAGCAGTCAATATTTGGCAACAGACCT	1588
1989	CATTGAAGAATATAAGACCAGTTTGAATAATAATCAAGCAAGCTATTTTATAGCTACAGACCT	2048
1589	CACGCTCTACTTTGAGAGGAGAACTGAATTTCTTTTGAACCTTGTCAGTAAAGGAGCAATACGA	1648
2049	AGCACTGTACATTAAGAGGCGGAGAAATTTTGTGAATTTAAGAAAAAATCAATTCAA	2108
1649	TTTGAACATCAAAAAACCATCGTGATATTTTCGATCAATGTTTAATCAGACGCTGTGACCT	1708
2109	TTTTGGAAGATCCCTCATCAAAAGAGTGTGTTTTGGCAATGCTGATGACAGCTTGTGATCT	2168
1709	TGGAGCGGTGACCAACCGGTGGGAGATCTCCAGACAGGTGGCAGAACTTTGTAAACCAGTGA	1768
2169	TTCTGCAATTTACAAAAACCCCTGGCCTATTCAACAACCGGATAGCAGAACTTTGTAGCAACTGA	2228
1769	GTTCCTTGAACAGGAGATCGGGAGAGATTTAGAGCTCAAACTCAGCTCTCCTTCAGCAATTTT	1828
2229	ATTTTTTGTATCAAGGAGACAGAGAGAAAAGAACTCAACATAGAACCCCACTGATCTAAT	2288
1829	TGATCGGAACCGGAAGGATCACTGCTCGGTTTGAACCTGGAGTGGATTGATGAGCATCTG	1888
2289	GACAGGGAGCAAAAAACAAATCCCAAGTATGCAAGTTGGTTCATAGATGCCATCTG	2348
1889	CATGCCCTTTGTATCAGGCACTGTGTGAAGGTCAACGTGAACCTGAAGCCGATGCTAGATTTC	1948
2349	CTTTGCAACTGTATGAGGCGCTTGACCCACGTGTTCAGAGGACTGTTTCCCTTTGCTAGATGG	2408

QY 1949 AGTAGCTACAAACAGAACTAAGTGGGAAGAGCT 1981
 Db 2409 CTGCAGAAAGAACAGGCAGAAATGCGAGCCCT 2441

RESULT 14

AAQ79715
 ID AAQ79715 standard; cDNA; 2645 BP.

XX AC AAQ79715;

DT 29-AUG-1995 (first entry)

XX DE Cyclic guanosine monophosphate specific phosphodiesterase.

XX KW Cyclic guanosine monophosphate specific diesterase; CGB-PDE;
 KW analysis; detection; binding proteins; signal transduction;
 KW immunisation; ss.

XX OS Homo sapiens.

XX FH Location/Qualifiers

FT CDS 12..2639

FT /*tag= a

FT /product= Cyclic guanosine monophosphate
 FT phosphodiesterase (composite).

XX PN W09428144-A.

XX PD 08-DEC-1994.

XX PF 27-MAY-1994; 94WO-US06066.

XX PR 27-MAY-1993; 93US-0068051.

XX PA (UNIV) UNIV WASHINGTON.

XX PI Beavo JA, Corbin JD, Ferguson KM, Francis SH, Kadlecsek A;
 PI Loughney K, Mcallister-lucas LM, Sonnenburg WK, Thomas MK;

XX WPI; 1995-022816/03.

XX DR P-PSDB; AAR66565.

XX CC Cyclic GMP-binding, cGMP-specific phosphodiesterase (CGB-PDE) DNA
 PT - also molis. (esp. monoclonal antibodies) able to bind CGB-PDE,
 PT and methods for identifying CGB-PDE modulators

XX PS Claim 18; Page 55-58; 77pp; English.

XX CC The recombinant production of the cyclic guanosine monophosphate
 CC specific phosphodiesterase (cGB-PDE) facilitates the analysis and
 CC structure of the CGB-PDE, particularly of activities involved in
 CC signal transduction. CGB-PDE binding proteins can be used for
 CC immunisation, for the purification, detection or quantification of
 CC CGB-PDE, or for modulating CGB-PDE activity. This is a
 CC constructed, composite CGB-PDE coding sequence.

XX SQ Sequence 2645 BP; 813 A; 537 C; 609 G; 686 T; 0 other;

Query Match 17.2%; Score 356.6; DB 16; Length 2645;
 Best Local Similarity 52.0%; Pred. No. 8e-100;
 Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;

QY 169 AGGATCGACGATTCAATGATGAATCGACAAGCTGACTGGATACAGACAAATCATAT 228

Db 751 AGGATCCTCGGTTCAATGCAAGATTGACCAAAATTACAGGCTTACAAAGACACAAAGCATTC 810

QY 229 TGTGCATGCCATCCGAAGCAGTGTGCTGAGATATTGGTGTGCCCAAGCGATAAATA 288

Db 811 TTTGTATGCCAATTAAAGATCATAGGAAGAGTTGTTGGTGTAGCCCGCCATCAACA 870

QY 289 AGATTCCCTG---AGGAGCTCCATTACTGAGATGATGAAAAAGTTATGCAGATGTATC 345

Db 871 AGAAATCAGGAAACGGTGGGACATTTACTGAAAAAGATGAAAAGGACTTTTGTCTGTATT 930
 QY 346 TTCCATTTTGGGAATCCCATATCTAAAGCTCAGCTCTTGTCTCCCTCAAGGAAAGAAAT 405
 Db 931 TGGCAATTTTGGGTATTGTTCTTCATAATGCTCAGCTCTATGAGACTTTCACCTGCTGGAGA 990
 QY 406 ATGAAAGAGCAGAGCTTTTGTAGAGTGGTGTAAATGACCTCTTTTGAAGAACAGACTGACC 465
 Db 991 ACAAGAGAAATCAGGTGCTGTGACCTTGTAGTTTAAATTTTGAAGAACAAACATCAT 1050
 QY 466 TGGAGAAAATTTCTCAAGAAAATAATGATCGGGGCCCAAACTCTGCTGAAATGTGAGCGCT 525
 Db 1051 TAGAAGTAATTTTGAAGAAAATAGCTGCCACTTATTCTCTTTCATGCAAGTGCAAAAT 1110
 QY 526 GTTCTGTTTTTACTCTCTAGAGACATCGAATACCAGTGGTGAATTTTACCAAAATCCTTTG 585
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Db 2546 CTGCAG 2578

RESULT 15
AAAX99393
ID AAAX99393 standard; cDNA; 2645 BP.
XX
AC AAAX99393;
XX
DT 09-NOV-1999 (first entry)
XX
DE Human cGMP-binding, cGMP-specific phosphodiesterase (cGB-PDE) cDNA.
DE
KW Cyclic guanosine monophosphate; cGMP; phosphodiesterase; cGB-PDE; enzyme;
KW antibody; Enzyme linked immunoabsorbant assay; ELISA; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12..2639
FT /*tag= a
FT /product= "cGB-PDE"
XX
FN US955583-A.
XX
PD 21-SEP-1999.
XX
PF 05-JUN-1995; 95US-0463949.
XX
PR 27-MAY-1994; 94US-0250847.
PR 27-MAY-1993; 93US-0068051.
PR 05-JUN-1995; 95US-0463949.
XX

(ICOS-) ICOS CORP.
PA (UYVA-) UNIV VANDERBILT.
PA (UNIW) UNIV WASHINGTON.
XX
PI Beavo JA, Corbin JD, Ferguson KM, Francis SH, Kadlecek A;
PI Loughney K, McAllister-lucas LM, Sonnenburg WK, Thomas MK;
XX WPI: 1999-539597/45.
DR P-PSDB; AAY14991.
XX
PT Antibodies specific for cGMP-binding, cGMP-specific
PT phosphodiesterase useful for detecting and modulating the enzyme
PS Example 6; Columns 49-56; 42pp; English.
XX
CC The invention provides nucleotide sequences encoding bovine and human
CC cyclic guanosine monophosphate (cGMP)-binding, cGMP-specific
CC phosphodiesterase (designated cGB-PDE). The enzymes can be recombinantly
CC expressed by standard recombinant methodology. Antibodies specifically
CC immunoreactive with the cGB-PDE enzyme may be used to modulate the
CC activity of the cGB-PDE enzyme. Additionally, they may be used in assays
CC (e.g. Enzyme linked immunoabsorbant assays (ELISAs)) to detect the
CC presence of the enzyme in biological samples. The present sequence
CC represents a cDNA encoding the human cGB-PDE enzyme.
XX
SQ Sequence 2645 BP; 813 A; 537 C; 609 G; 686 T; 0 other:
Query Match 17.2%; Score 356.6; DB 20; Length 2645;
Best Local Similarity 52.0%; Pred. No. 8e-100;
Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;
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QY 406 ATGAAGAAGCAGAGCTTTGCTAGAGTGTTAATGACCTCTTTTGAAGACAGACTGACC 465
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Job time : 508 secs

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 16:28:05 ; Search time 105 seconds
(without alignments)
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Title: us-09-663-542-2

Perfect score: 2078

Sequence: 1 ggccgagatgctgaagcag.....actaataactcgaggcatgc 2078

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1503.8	72.4	1784	4	US-09-595-514-2
3	1045.6	50.3	1982	3	US-09-226-741-4
4	1045.6	50.3	1982	4	US-09-595-514-4
5	356.6	17.2	2645	1	US-08-480-547A-22
6	356.6	17.2	2645	1	US-08-250-847B-22
7	356.6	17.2	2645	2	US-08-463-949A-22
8	356.6	17.2	2645	3	US-08-464-410A-22
9	356.6	17.2	2645	5	PCT-US94-06066-22
10	345.2	16.6	1982	1	US-08-480-547A-12
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13	345.2	16.6	1982	3	US-08-464-410A-12
14	345.2	16.6	1982	5	PCT-US94-06066-12
15	343.6	16.5	4474	1	US-08-480-547A-9
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17	343.6	16.5	4474	2	US-08-463-949A-9
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19	340.8	16.4	4474	5	PCT-US94-06066-9
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22	217.6	10.5	3195	2	US-08-951-648-5
23	217.6	10.5	3195	3	US-09-174-437-5
24	217.6	10.5	4389	2	US-08-951-648-3
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26	216.6	10.4	3789	1	US-07-872-644-2
27	216.6	10.4	3789	1	US-08-297-494-2

ALIGNMENTS

RESULT 1

US-09-226-741-2
; Sequence 2, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: HSPDE10A1
US-09-226-741-2

Query Match	Best Local Similarity	Score	DB	Length
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0;	Mismatches	0;	Indels	0;
Gaps	0;			
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DB	117	ACAGTGGTGAATTTACCAATCCTTTGAATTCATGTCGCCCAAGTGCAGTGGCTGATGC	176	
QY	617	TGAGAACAGTTTCAAGAACAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	676	
DB	177	TGAGAACAGTTTCAAGAACAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA	236	
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DB	237	CAGCATTCCTGAGCTGGTTGCTTCAACAGGCTTCCAGTGAACATCAGTGGCTTACCA	296	
QY	737	GGATCCGCGCTTTCATGACAGAGGAGACCATATCTGGTTTTCACATAGCATCTGTCT	796	
DB	297	GGATCCGCGCTTTCATGACAGAGGAGACCATATCTGGTTTTCACATAGCATCTGTCT	356	
QY	797	TTGTGTCCTATTTGGGAATAGCAACCAATAATTTGGAGTGGCTCAAGTGTAAACAG	856	
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QY	857	ACTTGATGGGAAACCTTTTGTATGATGACAGATCAACAGCTTTTGGAGCTTTTGTATCT	916	
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RESULT 2
US-09-595-514-2
; Sequence 2, Application US/09595514
; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version. 3.0
; SEQ ID NO 2
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDE10A1
US-09-595-514-2
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Query Match 72.4%; Score 1503.8; DB 4; Length 1784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 557 ACCAGTGGTGAATTTTACCAATCCTTTGAATTGATGTGCCCAAGTGCAGTCTGCTATGC 616
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Db 117 ACAGGTGGTGAATTTTACCAATCCTTTGAATTGATGTGCCCAAGTGCAGTCTGCTATGC 176
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|
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QY 617 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 676
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|
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Db 177 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 236
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|
|
QY 677 CAGCATTTGCTGAGCTGGTTCCTTCAACAGGCTTCCAGTGNACATCAGTGCCTACCA 736
|
|
|
Db 237 CAGCATTTGCTGAGCTGGTTCCTTCAACAGGCTTCCAGTGNACATCAGTGCCTACCA 296
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|
|
QY 737 GGATCCGCGCTTTTGCATGACAGGCGAGACAGATATCTGGTTCACATAGATCTGTCT 796
|
|
|
Db 297 GGATCCGCGCTTTTGCATGACAGGCGAGACAGATATCTGGTTCACATAGATCTGTCT 356
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|
|
QY 797 TTGTGTCCTTATTTGGAATAGCAACCAAAATTAATTTGGAGTGGCTCAAGTGTAAACAG 856
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|
|
Db 357 TTGTGTCCTTATTTGGAATAGCAACCAAAATTAATTTGGAGTGGCTCAAGTGTAAACAG 416
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|
|
QY 857 ACTTGATGGGAAACCTTTTGCATGATGACAGATCAACGACTTTTTCAGGCTTTTGTTCATCTT 916
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|
|
Db 417 ACTTGATGGGAAACCTTTTGCATGATGACAGATCAACGACTTTTTCAGGCTTTTGTTCATCTT 476
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|
QY 917 TTGTGGACTTGGCATCAACAACAATATATGATGATCAAGTGAAGAAGTCTCTGGGCCAA 976
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Db 477 TTGTGGACTTGGCATCAACAACAATATATGATGATCAAGTGAAGAAGTCTCTGGGCCAA 536
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QY 977 GCAGTCTGTGGCTCTTGTGATGCTATCATACCAACATGTTTCAAAAGCTGAAGTTGA 1036
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|
|
Db 537 GCAGTCTGTGGCTCTTGTGATGCTATCATACCAACATGTTTCAAAAGCTGAAGTTGA 596
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|
|
QY 1037 CAAAGTTTAAGCAGCCACATCCCTCTGGTGCAGAACTTCCCATCGATGACATTCATTT 1096
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Db 597 CAAAGTTTAAGCAGCCACATCCCTCTGGTGCAGAACTTCCCATCGATGACATTCATTT 656
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|
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Db 843 TCAGCTGATGTTCCGGATGTTAAACACATGCTGGGTTTCAAGACATCTTGACCGAGGTGGA 902
QY 1337 AATTTAGCGGTGATTGTGGATGCTGTGTCATGACCTCGACACAGCGGGAACCAAA 1396
Db 903 AATTTAGCGGTGATTGTGGATGCTGTGTCATGACCTCGACACAGCGGGAACCAAA 962
QY 1397 TGCCTTCAAGCTAAGATGGCTGTGCCCTGGCCCAACTCTATGGAACCTCTGTACCTT 1456
Db 963 TGCCTTCAAGCTAAGATGGCTGTGCCCTGGCCCAACTCTATGGAACCTCTGTACCTT 1022
QY 1457 GGAGCATCACATTTCAACACGGCGTGATGATCTTCAAGTGAGGCTCACAATATCTT 1516
Db 1023 GGAGCATCACATTTCAACACGGCGTGATGATCTTCAAGTGAGGCTCACAATATCTT 1082
QY 1517 TGCTAACCTGTCTCCCAAGGAATATAGTACCTTATGACGCTTTTGAAGAGCTCAATATT 1576
Db 1083 TGCTAACCTGTCTCCCAAGGAATATAGTACCTTATGACGCTTTTGAAGAGCTCAATATT 1142
QY 1577 GGCAACAGACCTCAGCGTGTACTTTGAGGAGA 1608
Db 1143 GGCAACAGACCTCAGCGTGTACTTTGAGGAGA 1174

RESULT 4

US-09-595-514-4

; Sequence 4, Application US/09595514

; Patent No. 6416991

; GENERAL INFORMATION:

; APPLICANT: Phillips, Stephen C.

; APPLICANT: Lanfeart, Jerry

; APPLICANT: Fawcett, Lindsay

; APPLICANT: Bandman, Olga

; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES

; FILE REFERENCE: PE-0623-1 CIP

; CURRENT APPLICATION NUMBER: US/09/595,514

; CURRENT FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: 09/226,741

; PRIOR FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 1982

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

; OTHER INFORMATION: HSPDE10A2

US-09-595-514-4

Query Match 50.3%; Score 1045.6; DB 4; Length 1982;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 557 ACCAGTGTGAAATTTACCAATCTTTGAATGATGTCGCCAAAGTGCAGTGTGATGC 616
|||
Db 123 ACAGTGTGAAATTTACCAATCTTTGAATGATGTCGCCAAAGTGCAGTGTGATGC 182
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QY 617 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 676
|||
Db 183 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCGACTGGCTTAATAATAA 242
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QY 677 CAGCATCTCAGCTGGTGTCTTCAACAGGCGTTCAGTGAACATCAGTATGCTTACCA 736
|||
Db 243 CAGCATCTCAGCTGGTGTCTTCAACAGGCGTTCAGTGAACATCAGTATGCTTACCA 302
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QY 737 GGATCCGGCTTTTGATGAGAGGAGACACAGATATCTGGTTTTCACATAAGATCTGTCT 796
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Db 303 GGATCCGGCTTTTGATGAGAGGAGACACAGATATCTGGTTTTCACATAAGATCTGTCT 362
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QY 797 TTGTGTCCTATTTTGAATAGCAACCAACCAATATTTGAGTGGCTCAAGTGTAAACAG 856
|||
Db 363 TTGTGTCCTATTTTGAATAGCAACCAACCAATATTTGAGTGGCTCAAGTGTAAACAG 422
|||
QY 857 ACTTGATGGGAACCTTTTGATGATGACATCAACGACTTTTTCAGGCTTTTTCATCTT 916
|||

; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,547A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565213land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32791
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 12..2636
; US-08-480-547A-22

Query Match 17.2%; Score 356.6; DB 1; Length 2645;
Best Local Similarity 52.0%; Pred. No. 1.6e-105;
Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;

QY 169 AGGATCGAGATCAATGATGAATCGACAAGCTGACTGGATACAGACAAAATCATTTAT 228
DB 751 AGGATCCTCGGTCAATGAGAGTTCACCAATTTACAGGCTACAGACACAAAGCATTC 810
QY 229 TGTGATGCTATCCCAAGCAGTGATGGTGAGATTTATGGTGGCCCAAGCGATAAATA 288
DB 811 TTGTATGCCAATTAGAAATCATAGGAGAGGTGGTGGTGGAGCCAGCCATCAACA 870
QY 289 AGATTCCTG---AAGGAGTCCATTTACTGAAGATGATGAAAAGTTATGCAATGATATC 345
DB 871 AGAAATCAGAAACGGTGGGACATTTACTGAAAAGATGAAAAGGACTTTGCTGCTTATT 930
QY 346 TTCCATTTTGTGAATCGCCATATCTAACGCTCAGCTCTTTGCTGCTCAAGAAAGAT 405
DB 931 TGGCAATTTGTGGTATTGTTCTCATTAATGCTCAGCTATGAGACTTCACTGCTGGAGA 990
QY 406 ATGAAAGAAGCAGAGCTTTGCTAGAGGTGTTAATGACCTCTTTGAAGAAGCAGCTGACC 465
DB 991 ACNAGAGAAATCAGTGGCTGCTGACCTTGCTAGTTAATTTTGAAGAACACAATCAT 1050
QY 466 TGGAGAAAATTGCAAGAAAATAATGCATCGGCCCCAAACTCTGCTGAAATGTGACGCT 525
DB 1051 TAGAAGTAATTTTGAAGAAAATAGTGCACATATTATCTCTTTTCATGCAAGTGCAGAAAT 1110
QY 526 GTTCTCTTTTACTCCTTAGAGGACATCGAATCACCAGTGGTGAATTTACCAATCTTTTG 585
DB 1111 GCACCAATTTTCAATGAGTGGATGAAGATTGCTCCGATCTTTTCTAGTGTGTTTCATG 1170
QY 586 AATTGATGTCCTCCAAAGTGCAGTGGCTGATGCTGAGAACAGTTTCAAGAAAGCATGGAG 645
DB 1171 AGTGTGAGGAATTTAGAAAATCATCTGATACATTTAACAGGGAACATGATGCAACAAA 1230
QY 646 AATCATCATCTCCGACTGGCTAATAAATAACAGCATTTGCTGAGCTGGTGTCTTCAACAG 705
DB 1231 TCAATTACATGTATGCTCAGTATGTCAAAAATACTATGGAACCACTTAAATATCCAGATG 1290
QY 706 GCCTTCCAGTGAACATCAGT-----GATGCCCTACCAGGATCCCGCTTTGTATGCCAGGC 760

DB 1291 TCAGTAAGGATAAAGATTTCCCTGGACAACACTGAAAATACAGGAAATGTAAACCACAGCT 1350
QY 761 AGACCAGATATCTGGTTTTCACATAAGATCTGTTCTTTGTGTCCTTATTTGGAAATAGCAA 820
DB 1351 GCATTTAGAAGTTTGTCTTTGTACACCTTATAAAAATGGAAGAAGATAAAGTTATAGGGG 1410
QY 821 CCACCAAAATAATTGGAGTGGCTCAAGTGTAAACAGACTTGATGGGAAACCTTTTTCATGA 880
DB 1411 TTTGCCAAGTCTGTTAATAAGATGGAGAGAATACTGGC--AAGGTTAAGCCTTTCAACCG 1468
QY 881 TGCAGATCAACGACTTTTGGAGCTTTTGTCACTTTTGTGGACTTTGGGATCAACACAC 940
DB 1469 AATGACGAACAGATTCTTGGAGCTTTTGTCACTTTTGTGGCTTTGGGATCCAGACAC 1528
QY 941 AATTATGTATGATCAAGTGAAGTCCCTGGGCAAGCAGTCTGTGGCTTCTTTCATGTGCT 1000
DB 1529 GCAGATGTATGAAGCAGTGGAGAGCCATGGCCAAGCAANTGTCACATTTGAGGTTCT 1588
QY 1001 ATCATACCATGCAACATGTTCAAAAGCTGAAGTTGACAAGTTTAAAGCGCCCAACATCC 1060
DB 1589 GTCGTATCATGCTTCAGCAGCAGAGGAAGAAACAGAGAGCTACAGTCGTTAGCGGCTGC 1648
QY 1061 TCTGGTGTC-----GAACTTCCCATCGATGACATTTCAATTTTTCATCATTCTCT 1111
DB 1649 TGTGGTGCCATCTGCCAGACCCCTTAAATTTACTGATTTAGCTTCAGTGACTTTGAGCT 1708
QY 1112 CGAGCTTGATGCCATGATCACAGCTGCTCTCCGGATGTTTCATGAGCTGGGGATGGTACA 1171
DB 1709 GTCTGATCTGGAACACAGCAGCTGTGTACAATTCGGATGTTTACTGACCTCAACCTTTG 1768
QY 1172 GAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGACAGTGAAGGAAACATA 1231
DB 1769 GAACTTCCAGATGAAACATGAGGTTCTTTGCAGATGGATTTTAAAGTGTAAAGAAGATTA 1828
QY 1232 TCGGATG---GTTCTATATCCACAACCTGGAGACATGCTTCAAGCTGTGTGACGCTGATGT 1288
DB 1829 TCGGAAGAATGTGGCTATCATTAATTTGGAGACATGCTTTAATACAGCTCAAGTGCATGT 1888
QY 1289 CGCGATGTTAAACACCTGCTGGGTTTCAAGACATCTTGACGAGGTGGAATTTTAGCGGT 1348
DB 1889 TGCTGCTCTAAAGCAGGCAAAATTCAGAACAGCTGACTGACCTGGAGATACTTGCATT 1948
QY 1349 GATTGTGGAGTGGCTGTGTATGACCTCGACACAGGGGAACCAACAATGCCCTTCCAAGC 1408
DB 1949 GCTGATTGCTGCACTAAGCCACGATTTGGATCACCGTGGTGTGAATAAATCTTACATACA 2008
QY 1409 TAGAGTGGCTGCTGCCCTGGCCCACTCTATGAACTCTGCTACCTGCTGAGCATCACCA 1468
DB 2009 GCGAAGTGAACATCCACTTGGCCAGCTTTACTG---CCATTTCAATCATGGAACACCATCA 2065
QY 1469 TTTCAACCACGCGCTGATGATCTTCAAGTGAAGGTGACAAATATCTTTGCTAACCTGTC 1528
DB 2066 TTTTGACCACTGCTGATGATCTTAAATAGTCCAGGCAATCAGATTTCTAGTGGCCTCTC 2125
QY 1529 CTCCAAGGAATAATGATGACCTTATGACGCTTTTGAAGCAGTCAATATGGAACAACAGACT 1588
DB 2126 CATTTGAAGAATAATAAGCACCGTTGAAAATAATAACAAGCAAGCTATTTTAGCTACAGACT 2185
QY 1589 CAGCTGTACTTTGACAGGAGAACTGAATTTCTTTGAACTTGTGAGTAAAGGAAATACGA 1648
DB 2186 AGCACTGTACATTTAAGGCGGAGAGAAITTTTGAACCTTATAGAAAATAATCAATTCAA 2245
QY 1649 TTGGAACATCAAAAACCATCTGATATATTTTCGATCAATGTTAATGACAGCTGTGACCT 1708
DB 2246 TTTGGAAGATCTTCATCAAAAGGAGTTGTTTTTGGCAATGCTGATGACAGCTTGTGATCT 2305
QY 1709 TGGAGCGTGACAAAACCGTGGGAGATCTCCAGACAGGTGGGAACTTTGTAAACCAAGTGA 1768
DB 2306 TTTCTGCAATTTACAAAACCGCTTGGCTTATTCACAACCGATAGCAAGAACTTGTAGCACTGA 2365
QY 1769 GTTCTTCGAACAGGAGATCGGGAGAGATTAGAGCTCAAACTCACCTCCTTCACCAATTTT 1828
DB 2366 ATTTTGTGATCAAGGAGACAGAGAGAAAAGAACTCAACATAGAACCCCACTGATCTAAT 2425

Qy 1232 TCGATG---GTTCTATACACAACTGGAGACATGCGCTTCAACGTGTGTCAGCTGATGTT 1288
Db 1829 TCGAAGAATGTTGCCCTATCATATATGGAGACATGCGCTTTAAATACAGCTAGTGCATGTT 1888
Qy 1289 CGCGATGTTAACCACTGCTGGTATTCAAGACATCTGACGAGGTGGAAATTTTAGCGGT 1348
Db 1889 TGCTGCTCTAAAGCAGGCAAAATTCAGACAAGCTGACTGACCTGGAGATACATTGGCAT 1948
Qy 1349 GATTGTGGGATGCTGTGTCATGACCTCGACCAAGGGGAAACCAACAAATGCTTCCAAAGC 1408
Db 1949 GCTGATTGCTGCATAAGCCAGCATTTTGGATCACCGGTGTGTAATAACTCTTACATACA 2008
Qy 1409 TAAGAGTGGCTCTGCCCTGGCCCACTCTATGGAACTCTGCTACCTTGGAGATACCA 1468
Db 2009 GCGAAGTGAACATCCACTGCCAGCTTTTACTG---CCATTCATCATGGAACACCATCA 2065
Qy 1469 TTTCACCAACCCCGTGATGCTCTTCAAGTGGAGGCTCACAAATATCTTTGCTAACCTGTC 1528
Db 2066 TTTTGACCACTGCTGATGCTTCTTAATAGTCCAGGCAATCAGATTCAGTGGCCCTCTC 2125
Qy 1529 CTCAAGGAATATAGTGACCTTATGACGCTTTTGAAGCAGTCAATATTTGGCAACAGACCT 1588
Db 2126 CATTAAGAATATTAAGACCACTGTTGAAATTAATCAAGCAAGCTATTTTAGCTACAGACCT 2185
Qy 1589 CACGCTGTACTTTAGAGGAGAACTGAATCTTTTGAACCTTGTCACTAAGAGAAATAGA 1648
Db 2186 AGCACTGTACATTAAGAGGAGGAGAAATTTTGAACCTTATAAGAAAAATCAATCAAA 2245
Qy 1649 TTGAACATCAAAACCATCGTGATATATTTTCGATCAATGTTAATGACAGCTGTGACCT 1708
Db 2246 TTTTGAAGATCCTCATCAAGAGAGTTGTTTGGCAATGCTGATGACAGCTTGTGATCT 2305
Qy 1709 TGGAGCGGTGACCAAAACCGTGGGAGATCTCCAGAGGTGGCAGAACTTGTAAACAGTGA 1768
Db 2306 TTTGCAATTAACAAACCCCTGGCCCTATTCAACAACGGATAGCAGAACTTGTAGCAACTGA 2365
Qy 1769 GTTCTTGAACAAGAGATCGGAGAGATTAAGACTCAAACTCACTCTTCCAGCAATTT 1828
Db 2366 ATTTTGTGATCAAGGACAGAGAGAGAAAGAACTCAACATAGAACCCACTGATCTAAT 2425
Qy 1829 TGATCGGAACCGGAGGATGACCTGCTCGGTTTCCAACTGGAGTGGATGATGATGATCTG 1888
Db 2426 GAACAGGAGNAGAAAAACAAATCCCAAGTATCCAACTTGGGTTTATAGATGCCATCTG 2485
Qy 1889 CATGCCCTTGTATCAGGCACTGTGTAAGGTCAAGCTGAACTGAAGCGATGCTAGATTC 1948
Db 2486 CTTGCAACTGTATGAGCCCTGACCCAGGTGTCAGAGGACTGTTTCCCTTTGCTAGATGG 2545
Qy 1949 AGTAGCTACAACAAGAGATAGTGGGAGAGCT 1981
Db 2546 CTGCAAGAAGAACAGGAGAAATGGCAGGCCCT 2578

RESULT 7
US-08-463-949A-22
; Sequence 22, Application US/08463949A
; Patent No. 5955583
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharon H.
; APPLICANT: Kadlecik, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5955583and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 2645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 12..2636
US-08-463-949A-22

Query Match 17.2%; Score 356.6; DB 2; Length 2645;
Best Local Similarity 52.0%; Pred. No. 1.6e-105;
Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;
Qy 169 AGGATCGACGATTCGAATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGAT 228
Db 751 AGGATCGGATTCGAATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGAT 810
Qy 229 TGTGATGCTTCATCCGAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 288
Db 811 TTTGATGCTTCATCCGAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 870
Qy 289 AGATTCCTG---AAGGAGCTCCATTTACTGAAGATGATGATGATGATGATGATGATGATGAT 345
Db 871 AGAATCAGGAACGGTGGGACATTTACTGAAAAGATGAAAAGGACTTTGCTGCTTATT 930
Qy 346 TTCCATTTTGGGATCCCATATCTAACGCTCAGCTCTTTGCTGCTCCCTCAAGGAAGAT 405
Db 931 TGGCATTTTGGGATTTGTTCTCATAATGCTCAGCTCTATGAGACTTCACTGCTGGAGA 990
Qy 406 ATGAAAGACGACAGCTTTGCTAGAGTGGTGTATGACCTCTTTGAAGAACAGACTGACC 465
Db 991 ACAAGAGAAATCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1050
Qy 466 TGGGAAATTTGTCAAGAAATAATATGATCGGGCCCAAACTGCTGCTGCTGCTGCTGCTGCT 525
Db 1051 TAGAAGTAATTTTGAAGAAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
Qy 526 GTTCTGTTTACTCTAGAGGACATCGAATCACCAGTGTGTAATTTTACCAATCTCTTTG 585
Db 1111 GCACATTTTCTAGTGGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1170
Qy 586 AATTGATGCTCCCAAGTGCAGTGTGATGCTGAGAACATTTTCAAGAACAGCATGGAGA 645
Db 1171 AGTGTGAGGAATTAGAAAAATCATCTGATACATTAACCAAGGGAACATGATGCAACAAA 1230
Qy 646 AATCATCATCTCCGACTGGCTTAATAATAACAGCATTTGCTGAGCTGCTGCTGCTGCTGCT 705

Db	1231	TCAATTACATGATGCTCAGTATGCTCAAAATACTATGGAAACCACTTAAATATCCAGATG	1290
Qy	706	GCCTTCAGGTGAACATCAGT-----GATGCTTACCAGGATCCGCGCTTTTGATCGACAGGC	760
Db	1291	TCAGTAAGGATAAAAGATTTCCCTTGGACAACCTGAAATACAGGAATGTAAACCAGCAGT	1350
Qy	761	AGACCAGATATCTGGTTTTCACATAAGATCTGTCTTGTGTCCTTATTTGGATATAGCAA	820
Db	1351	GCATTAGAAGTTTGCCTTTGTGACACCTATAAAAAATGGAAAAGAGATAAAGTTATATAGGG	1410
Qy	821	CCACCAATAATTGGAGTGCCTCAAGTGTAAACAGACTTTGATGGGAAACCTTTTGATGA	880
Db	1411	TTTGCCAACTTGTTTAATAAGATGGAGAGAAATCTGCG--AAGTTAAGCCTTTCACCCG	1468
Qy	881	TGCAGATCAACGACTTTTTTGAGGCTTTTGTGACTTTTGTGGACTTGGCATCAACAACAC	940
Db	1469	AAATGACGAACAGTTTCTGGAAGCTTTTGTGTCATCTTTTGTGGCTTGGGATCCGAAACAC	1528
Qy	941	AATTATCTATGATCAAGTGAAGAAGTCTCTGGGCCAAGCACTCTGTGGCTCTTGTATGGCT	1000
Db	1529	GCAGATGTTGAAGCAGTGGAGAGAGCCATGGCCAGCAAAATGGTCATTTGAGAGTTCT	1588
Qy	1001	ATCATACCATGCAACATGTTTCAAAGCTGAAGTTGACAAGTTTAAAGSCAGCCAAACATCCC	1060
Db	1589	GTCGTATCATGCTTCAGCAGCAGAGGAAGAAACAAGAGACTACAGTCGTTAGCGGCTGC	1648
Qy	1061	TCGTGGTGTCA-----GAACTTGCCATCGATGACATTCATTTTGTGACTTTTCTCT	1111
Db	1649	TGTGTTGCCATCTGCCAGACCCCTTAAATTTACTGACTTTTAGCTTCAGTGACATTTGAGCT	1708
Qy	1112	CGAGTTTGATGCCATGATCATCAGCTGCTCTCCGGATGTTTCATGGAGCTGGGATGGTATCA	1171
Db	1709	GTCTGATCTGGAACACGACACTGTGTACAATTCGGATGTTTACTGACCTCAACCTTGTGCA	1768
Qy	1172	GAATTTAAATTTGACTATCAGACACTGTGTAGTGGCTTTTGCAGAGTGAGGAAAACATA	1231
Db	1769	GAACTTCCAGATGAACATCAGGTCTCTTCGACATGGATTTTAAAGTGTAAAGAAGAAATTA	1828
Qy	1232	TCGGATG--GTTCTATACCACAACCTGGAGACATGCTTCAACGTGTGTGACGTGATGTT	1288
Db	1829	TCGGAAGAATGTTGCCCTATCATAAATGGAGACATGCCTTTAATACAGCTCAGTGCATGTT	1888
Qy	1289	CGGATGTTAAACACTGCTGGGTTTCAAGACATTTCTGACGGAGGTGGAATTTTACGGGT	1348
Db	1889	TGCTGTCTTAAAGCAGGCAAAAATTCAAGAACAGCTGACTGACCTGGAGATACCTGCATT	1948
Qy	1349	GATTTGGGATGCTGTGTACAGCTTCGACCACAGGGGAACCAACAATGCCCTTCCAAGC	1408
Db	1949	GCTGATTTGCTACTAAGCCACAGATTTGGATCACCGTGTGTAATCTTTACATACA	2008
Qy	1409	TAAAGTGGCTGTGCCCTGGCCCCAATCTATGAAACCTCTGTACCTTGGAGCATCACCA	1468
Db	2009	GCGAAGTGAACATCCACTTCCCGAGCTTTACTG---CCATTCAATCATGGAACACCATCA	2065
Qy	1469	TTTCAACCCGCGTGTATGATCTTCAAAGTGAAGGTGCACAATATCTTGTCTTAACCTGTC	1528
Db	2066	TTTGTACCATGCTGATGATCTTAATAGTCAGGCAATTCAGATTTCTCAGTGGCCTCTC	2125
Qy	1529	CTCCAAGGAATATAGTACCTTATGACGCTTTTGAAGCAGCTCAATATTTGGAACAGACCT	1588
Db	2126	CATTGAAGATAATAAGACCAGTTGAAATAAATCAAGCAGCTATTTAGCTACAGACCT	2185
Qy	1589	CAGCTGTACTTTGAGAGGAGAACTGAATCTTTTGAACCTTGTCAAGTGAAGGAGAAATACA	1648
Db	2186	AGCACTGTACATTTAAGAGCGCAGGAGAAATTTTGAACCTTATGAAGAAAAATCAATTCAA	2245
Qy	1649	TTGGAACATCAAAAAACATCGTGTATATTTTCGATCAATGCTTAAATCAGACGCTGTGACCT	1708
Db	2246	TTTGGAGATCTCATCAAAAGAGATGTGTTTTGGCAATGCTGATGACAGCTTTGTGATCT	2305
Qy	1709	TGGAGCGGTGACCAACCGTTGGAGATCTCCAGACAGGTGGCAGAACTTTGTAAACCAAGTGA	1768

2306	TTCGCAATTCACAAACCCCTGGCCTATTCAACAACGGATAGCAGAACTTGTGACAACTGA	2365
1769	GTTCTTCGAACAAGGAGATCGGAGAGATTAGAGCTCAAACTCACCTCCTTCAGCAATTTT	1828
2366	ATTTTGTGATCAAGGACAGACAGAGAAAGAACTCAACATAGAACCCTATGATCTAAT	2425
1829	TGATCGGACCCGAAGGATCAACTGGCTTCGGTTTGCACATGGAGTGGATTGCATAGACTCTG	1888
2426	GAACAGGGAGAAGAAAACAAAATCCCAAGTATGCAAGTTTGGGTTTCATAGATGCCATCTG	2485
1889	CATGCGCTTTCTATTACCGACCTGCTGAAGGTCACGTTGAACCTGAACCGATGCTAGACTTC	1948
2486	CTTTCGAACGTATGAGGCCCTGACCCACGTCGTACAGAGGACTGTTTCCCTTTGCTAGATGG	2545
1949	AGTAGCTACAAACAGAGTAAGTGGGAAGAGCT	1981
2546	CTGCAGAAAGAACAGGCAGAGAAATGGCAGGCCCT	2578

RESULT 8

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US-08-464-410A-22
; Sequence 22, Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecak, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: Mcallister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,410A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037119and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2636
US-08-464-410A-22

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Query Match

17.28: score 356.6: DB 3: Length 2645:

[illegible]

RESULT 10

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RESOLVING TO
US-08-480-547A-12
; Sequence 12, Application US/08480547A
; Patent No. 5652131
; GENERAL INVENTION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecck, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:

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;
;      0000
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/98/480-547A
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; TELE: 23-3636
; INFORMATION FOR SEQ ID NO: 12:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: cdna
US-08-480-547A-12

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	Best Local Similarity	52.3%;	Pred. No. 6.8e-102;		
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Db	232	AGATCTCGGTTCAAT	GCGAAGATTGACCAAAATTACAGGCTACAGACACAAGCATTC		291
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532	Db	TAGAAATTTTCAAGAAATAGCTCCCACTATTATCTCTTTTCATGCAAGTCAGAAAT	591
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832	Db	GCATTTAGAAGTTTGCCTTTGTGTACACCTATAAAAAATGGAAAGAAGATAAAAGTTATAGGG	891
821	Qy	CCACCAATAATTGGAGTGCCTCAAGTGTAAACAGACTTGTATGGGAAACCTTTTGTATGA	880
892	Db	TTTGCCCAACTTGTTAATAAGATGGAGAGAAATCTGCG---AAGTTTAAGCCTTTCAACCG	949
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950	Db	AAATGAGCAACAGTTTCTGGAAGCTTTTGTCACTCTTTTGTGGCTTGGGGATCCAGAACAC	1009
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1010	Db	GCAGATGATGAAGCAGTGGGAGAGCCATGGCCAGCAAAATGGTCACATTTGAGGGTTCT	1069
1001	Qy	ATCATACATGCACATGTTCAAAAGCTGAAGTTGACAAGTTTAAAGGCACCAACATCCC	1060
1070	Db	GTCTGATATGCTTCACACACGAGGAAGAAACAAGAGACTACAGTCTGTACGGGCTGC	1129
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1130	Db	TGTGCTGCCATCTGCCACAGACCCCTTAAAAATTACTGACTTTAGCTTCAGTTCAGTTCAGCT	1189
1112	Qy	CGAGTTGATGCCATGATACAGCTGCTCTCCGATGTTTCATGAGCTGGGGATGGTACA	1171
1190	Db	GTCTGATCTGGAACACAGCACTGTGTACAATTTCCGATGTTTACTGACCTCAACCTTGTGCA	1249
1172	Qy	GAAATTTAAAATTGACTATGAGACACTGTGTAGTGGCTTTTGACAGTGGAGAAAACATA	1231
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1232	Qy	TCGGATG---GTTCTATACCAACTGGACATGCGCTTCAAGCTGTGTTCAGCTGATGTT	1288
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1370	Db	TGCTGCTCTTAAAGACGGGAAAATTTAGAACAGCAAGCTGACTGACTGGAGATACTTGCA	1429

Query Match	16.6%	Score 345.2;	DB 2;	Length 1982;
Best Local Similarity	52.3%	Pred. No. 6.8e-102;		
Matches	918;	Conservative 0;	Mismatches 813;	Indels 25; Gaps 6;
Qy	169	AGGATCCACCATTC	AAATGATGAATC	CACAAGCTGACTGGATCAACAGCAAAATCAATTAT 228
Db	232	AGGATCTCGGTTCA	ATGCGAAGCTTGCCCAAT	TACAGGCTACAGCACACAAAGCATTC 291
Qy	229	TGTGCATGCCTATCC	GAAGCAGTGATGGTGAGAT	TATTGGTGTGGCCCAAGCGATAAATA 288
Db	292	TTTGTATGCCAATT	TAAACAATCATAGGCAAGAGG	TGTGGTGTAGCCCAAGGCCATCAACA 351
Qy	289	AGATTCTCGTGG	TTTACTGAGAGTATG	AAAGAGTTATGCAGATGTATC 345
Db	352	AGAAATCAGGAAC	CGGTGGGACATTTTACTG	AAAAGATGAAGAGACTTTGCTGCTTTAT 411
Qy	346	TTCCATTTTGTGG	AATCCCATATCTAACGCT	CAGCTCTTTGTGCTCAAGGAAGAANT 405
Db	412	TGGCATTTTCTGG	TATGTTCTTCATATGCT	CAGCTCTATGAGACTTACTGCTGGAGA 471

Qy 406 ATGAAGAAGCAGAGCTTTGGTAGAGTGGTTAATGACCTCTTTGAAGAAGCAGACTGACC 465
Dy 472 ACAAGAGAATCAGTGTCTGCTGACCTTGCTAGTTTAAATTTTGAAGAAGCAACATCAT 531
Qy 466 TGGAGAAATTTGCAAGAAATATATGATCGGGCCCAAACTCTGCTGAAATGTGAGCGCT 525
Dy 532 TAGAAGTAAATTTTGAAGAAGAAATAGTCCACATATATCTCTTTCATGCAAGTGCAGAAAT 591
Qy 526 GTTCTGTTTACTCCTAGAGACATCGAATCACAGTGGTGAATTTTACCAAAATCCCTTG 585
Dy 592 GCACCAATTTTCATAGTGGATGAAGATTGCTCCGATCTCTTTTCTAGTGTGTTTACATGG 651
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Dy 652 AGTGTAGGATTAAGAAATCATCTGATACATTAACAAGGAACATGATGCAACAA 711
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Dy 712 TCAATTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 771
Qy 706 GCCTTCCAGTGAACA-----TCAGTGTGCTTACCAGGATCCGCGCTTTGATGAGGCG 760
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Dy 832 GCATTAGAAGTTGCTTTGTACACCTATAAATAATGGAAGAAGAAATTAAGTTATAGGG 891
Qy 821 CCACCAATATTTGAGTGGCTCAAGTGTAAACAGACTTGTGAGCTGGGAACCTTTTGATGA 880
Dy 892 TTTGCCCACTTTTAAAGATGAGGAGATATCTGCG--AAGGTTAAGCCTTTTCAACCG 949
Qy 881 TGCAGATCAACGACTTTTGGAGCTTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 940
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Dy 1130 TGTGCTGCTTCTGCCAGACCTTTAAATTTAGTCTTTAGCTTTAGCTTTAGCTTTAGCTTT 1189
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RESULT 13

US-08-464-410A-12

; Sequence 12, Application US/08464410A

; Patent No. 6037119

; GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.

; APPLICANT: Corbin, Jackie D.

; APPLICANT: Ferguson, Kenneth M.

; APPLICANT: Francis, Sharron H.

; APPLICANT: Kadlecik, Ann

; APPLICANT: Loughney, Kate

; APPLICANT: McAllister-Lucas, Linda M.

; APPLICANT: Sonnenburg, William K.

; APPLICANT: Thomas, Melissa K.

; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific

; TITLE OF INVENTION: Phosphodiesterase Materials and Methods

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 S. Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,410A

; FILING DATE: June 5, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6037119and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/32705

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06066
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/068,051

FILING DATE: 27-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32083

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1982 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US94-06066-12

Query Match 16.6%; Score 345.2; DB 5; Length 1982;

Best Local Similarity 52.3%; Pred. No. 6.8e-102;

Matches 918; Conservative 0; Mismatches 813; Indels 25; Gaps 6;

Qy	169	AGGATCGACGATTC	CAATGATGAAATCG	GACAGCTGAC	TGGATACAA	GACAAATCA	TATAT	228
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1891.8	91.0	2889	10	US-09-891-216-18	Sequence 18, Appli
4	1891.8	91.0	4656	10	US-09-891-216-6	Sequence 6, Appli
5	1664.8	80.1	2261	10	US-09-891-216-7	Sequence 7, Appli
6	1503.8	72.4	1784	9	US-10-094-168B-2	Sequence 2, Appli
7	1045.6	50.3	1982	9	US-10-094-168B-4	Sequence 4, Appli
8	388.8	18.7	426	10	US-09-891-216-4	Sequence 4, Appli
9	388.8	18.7	426	10	US-09-891-216-11	Sequence 11, Appli
10	356.6	17.2	2645	9	US-10-115-515-22	Sequence 22, Appli
11	345.2	16.6	1982	9	US-10-115-515-12	Sequence 12, Appli
12	343.6	16.5	4474	9	US-10-115-515-9	Sequence 9, Appli
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16	216.6	10.4	3789	10	US-09-883-825-42	Sequence 42, Appli
17	216.6	10.4	4131	10	US-09-883-825-38	Sequence 38, Appli
18	215.6	10.4	1107	9	US-10-115-515-17	Sequence 17, Appli
19	213.8	10.3	3044	10	US-09-883-825-44	Sequence 44, Appli

20	213.8	10.3	4171	12	US-10-094-989-1	Sequence 1, Appli
21	213.8	10.3	4240	9	US-09-954-531-971	Sequence 971, App
22	201.6	9.7	3606	10	US-09-321-801-14	Sequence 14, Appl
23	200.8	9.7	341	10	US-09-891-216-10	Sequence 10, Appl
24	198.4	9.5	3219	9	US-10-202-107-1	Sequence 1, Appli
25	181	8.7	3231	9	US-10-175-523-149	Sequence 149, App
26	174	8.4	3221	10	US-09-815-825-19	Sequence 19, Appl
27	159.4	7.7	2060	9	US-10-115-515-11	Sequence 11, Appl
28	144.4	6.9	319	10	US-09-891-216-19	Sequence 19, Appl
29	144.4	6.9	401	10	US-09-891-216-1	Sequence 1, Appli
30	132	6.4	132	9	US-10-040-570B-1	Sequence 1, Appli
31	107.6	5.2	467	9	US-09-918-995-33958	Sequence 33958, A
32	103.6	5.0	365	10	US-09-960-352-10616	Sequence 10616, A
33	103.6	5.0	449	10	US-09-960-352-12064	Sequence 12064, A
34	102	4.9	245	9	US-09-535-459-1991	Sequence 1991, Ap
35	100.4	4.8	244	9	US-09-535-459-1855	Sequence 1855, Ap
36	100.4	4.8	246	9	US-09-535-459-2010	Sequence 2010, Ap
37	100.4	4.8	259	9	US-09-535-459-2019	Sequence 2019, Ap
38	100.4	4.8	263	9	US-09-535-459-2004	Sequence 2004, Ap
39	100.4	4.8	267	9	US-09-535-459-1987	Sequence 1987, Ap
40	100.4	4.8	269	9	US-09-535-459-1994	Sequence 1994, Ap
41	100.4	4.8	269	9	US-09-535-459-2015	Sequence 2015, Ap
42	100.4	4.8	271	9	US-09-535-459-2012	Sequence 2012, Ap
43	100.4	4.8	273	9	US-09-535-459-1976	Sequence 1976, Ap
44	100.4	4.8	273	9	US-09-535-459-2011	Sequence 2011, Ap
45	100.4	4.8	274	9	US-09-535-459-1980	Sequence 1980, Ap

ALIGNMENTS

RESULT 1

US-09-891-216-8
; Sequence 8, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(2502)
; OTHER INFORMATION: n = A,T,C or G
US-09-891-216-8

Query Match	99.0%	Score 2058;	DB 10;	Length 2502;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2058;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	6	GAGATGCTGAGCAGGCAAGACCTTTATTCAGAAATGCTCAGTGCACACAGTGG	65	
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QY	66	AAAAAGGTGAAATACACAGACTGTCCAAATCTCTGGGGCTCTTTGGCTGAAAAACAG	125	
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Db 320 GATGAATCGACAGCTGACTGGATACAGACAAAATCATTATTGTGCATGCCATCCGA 379
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Qy 546 GACATCGAATCACCAGTGGTGAATTTACCAAAATCTTTGAATTCATGCTCCCAAGTGC 605
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Qy 726 GATGCTACAGGATCCGCGCTTTGATGCAGAGCAGACCATCATCTGTTTTCACATA 785
Db 860 GATGCTACAGGATCCGCGCTTTGATGCAGAGCAGACCATCATCTGTTTTCACATA 919
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Qy 1806 AAATCTACTCTCTCAGCAATTTTGTATCGGAACCGGAAGGATGAATCTCCCTCGGTTGCA 1865
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Qy 2046 AAGGAACAGCAACTAA 2063
Db 2180 AAGGAACAGCAACTAA 2197

RESULT 2

US-09-891-216-9
; Sequence 9, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221

[illegible]

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: Sequence 18, Application US/09891216
: Patent No. US20020103120A1
: GENERAL INFORMATION:
: APPLICANT: Ramakrishnan, Shyam
: TITLE OF INVENTION: Regulation of Human
: TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
: FILE REFERENCE: 02973.00511
: CURRENT APPLICATION NUMBER: US/09/891,216
: CURRENT FILING DATE: 2001-06-26
: PRIOR APPLICATION NUMBER: US 60/213,998
: PRIOR FILING DATE: 2000-06-26
: PRIOR APPLICATION NUMBER: US 60/293,221
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: PCT/EP01/07289
: PRIOR FILING DATE: 2001-06-26
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 18
: LENGTH: 2889
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-891-216-18

Query Match      91.0%; Score 1891.8; DB 10; Length 2889;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2029 CCAGTCTTATGGTAGCCAAAGGACGAGAACTAA 2063
Db 2793 CCAGTCTTATGGTAGCCAAAGGACGAGAACTAA 2827

RESULT 4

US-09-891-216-6
; Sequence 6, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-891-216-6

Query Match 91.0%; Score 1891.8; DB 10; Length 4656;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1549 TTATGACGCTTTTGAAGCAGTCAATATTTGGGCAACAGACCTCAGCTGTACTTTGAGAGA 1608
Db 2789 TTATGACGCTTTTGAAGCAGTCAATATTTGGGCAACAGACCTCAGCTGTACTTTGAGAGA 2848
QY 1609 GAACTGAACTTCTTGAACCTTGCAGTAAAGGAGATACGATTTGGGAACATCAAAAACCATC 1668
Db 2849 GAACTGAACTTCTTGAACCTTGCAGTAAAGGAGATACGATTTGGGAACATCAAAAACCATC 2908
QY 1669 GTGATATATTTGATCAATGTTTAAATGACAGCTGTGACCTTTGGAGCGGTGACCAACCTG 1728
Db 2909 GTGATATATTTGATCAATGTTTAAATGACAGCTGTGACCTTTGGAGCGGTGACCAACCTG 2968
QY 1729 GGGAGATCTCCAGACAGGTGGCAGAACCTTGTAAACAGTGTGTTCTTGAACAGGAGATC 1788
Db 2969 GGGAGATCTCCAGACAGGTGGCAGAACCTTGTAAACAGTGTGTTCTTGAACAGGAGATC 3028


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Qy 1706 CCTTGGAGCCGTGACCAAAACCGTGGGAGATCTCCAGACAGGTGCAGAACTTGTAAACCAG 1765
Db 1539 CCTTGGAGCCGTGACCAAAACCGTGGGAGATCTCCAGACAGGTGCAGAACTTGTAAACCAG 1598
Qy 1766 TGAGTCTCTCGAAACAGGAGATCGGAGAGATTTAGAGCTCAAACTCACTCCTTCAGCAAT 1825
Db 1599 TGAGTCTCTCGAAACAGGAGATCGGAGAGATTTAGAGCTCAAACTCACTCCTTCAGCAAT 1658
Qy 1826 TTTTGATCGGAACCGGAGATGAACCTGCCCTGCTTGCACCTGGAGTGGATTGATAGCAT 1885
Db 1659 TTTTGATCGGAACCGGAGATGAACCTGCCCTGCTTGCACCTGGAGTGGATTGATAGCAT 1718
Qy 1886 CTGCATGCCCTTTGATCAGGCACCTGGTGAAGGTCAACCGTGAACCTGAAGCCGATGCTAGA 1945
Db 1719 CTGCATGCCCTTTGATCAGGCACCTGGTGAAGGTCAACCGTGAAGCCGATGCTAGA 1778
Qy 1946 TTCAGTAGCTACAACAGAGTAAGTGGGAGAGCTACACCAAAAGACTGCTGGCCTC 2005
Db 1779 TTCAGTAGCTACAACAGAGTAAGTGGGAGAGCTACACCAAAAGACTGCTGGCCTC 1838
Qy 2006 AACTGCCCTCATCCTCCCTCCCTGCCAGTGTATGGTAGCCCAAGGAAGACAGAACTAA 2063
Db 1839 AACTGCCCTCATCCTCCCTCCCTGCCAGTGTATGGTAGCCCAAGGAAGACAGAACTAA 1896

RESULT 6
US-10-094-168B-2
; Sequence 2, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PP-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094.168B
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A1
US-10-094-168B-2

Query Match 72.4%; Score 1503.8; DB 9; Length 1784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 557 ACCAGTGGTGAATTTACCAAACTCCTTTGAATTTGATGTGCCCAAGTGCAGTGCCTGATGC 616
Db 117 ACAGTGGTGAATTTACCAAACTCCTTTGAATTTGATGTGCCCAAGTGCAGTGCCTGATGC 176
Qy 617 TGAGAACAGTTTCAAAGAAAGCATGGAGAAATCATCATCTACCTCCGACTGGCTTAATAATAA 676
Db 177 TGAGAACAGTTTCAAAGAAAGCATGGAGAAATCATCATCTACCTCCGACTGGCTTAATAATAA 236
Qy 677 CAGCATTTGCTGAGCTGGTGTGCTTCAACAGGCCCTTCCAGTGAACATCAGTGAATGAGTACCA 736
Db 237 CAGCATTTGCTGAGCTGGTGTGCTTCAACAGGCCCTTCCAGTGAACATCAGTGAATGAGTACCA 296
Qy 737 GGATCCGCGCTTTGATGCAGAGGAGACCATATCTGGTTTTTCCACATAAGATCTGTCT 796
Db 297 GGATCCGCGCTTTGATGCAGAGGAGACCATATCTGGTTTTTCCACATAAGATCTGTCT 356
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Qy 797 TTGTGTCCTTATTTGGGAATAGCAACCAACCAAAATAAATTGGAGTGGCTCAAGTGTAAACAG 856
Db 357 TTGTGTCCTTATTTGGGAATAGCAACCAACCAAAATAAATTGGAGTGGCTCAAGTGTAAACAG 416
Qy 857 ACTTGATGGGAAACCTTTTGGATGATGAGATCAACAGCTTTTTCGAGCTTTTTCATCTTT 916
Db 417 ACTTGATGGGAAACCTTTTGGATGATGAGATCAACAGCTTTTTCGAGCTTTTTCATCTTT 476
Qy 917 TTGTGGACTTTGGCATCAACACACAATTTATGATGATCAAGTGAAGAAGTCTCTGGGCCAA 976
Db 477 TTGTGGACTTTGGCATCAACACACAATTTATGATGATCAAGTGAAGAAGTCTCTGGGCCAA 536
Qy 977 GCAGTCTGTGGCTCTTGTGATGCTATCATACCATGCAACATGTTCAAAGCTGAAGTTGA 1036
Db 537 GCAGTCTGTGGCTCTTGTGATGCTATCATACCATGCAACATGTTCAAAGCTGAAGTTGA 596
Qy 1037 CAAGTTTTAAGCGACGCAACATCCCTCTGGTGTGAGAACTTCCCATCGATGACATTCATTT 1096
Db 597 CAAGTTTTAAGCGACGCAACATCCCTCTGGTGTGAGAACTTCCCATCGATGACATTCATTT 656
Qy 1097 TGATGACTTTTCTCTCGACGTTGATGGCATGATCACAGCTGCTCTCCGGATGTTTCATGGA 1156
Db 657 TGATGACTTTTCTCTCGACGTTGATGGCATGATCACAGCTGCTCTCCGGATGTTTCATGGA 716
Qy 1157 GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 1216
Db 717 GCTGGGATGGTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 776
Qy 1217 AGTGAGGAAAACTATCGGATGTTCTATACCAACCTGGAGACATGCTTCAACGTGTG 1276
Db 777 AGTGAGGAAAACTATCGGATGTTCTATACCAACCTGGAGACATGCTTCAACGTGTG 836
Qy 1277 TCAGCTGATGTTCCGCGATGTTAAACACCTGCTGGGTTTCAAGACATTTCTGACCGAGTGA 1336
Db 837 TCAGCTGATGTTCCGCGATGTTAAACACCTGCTGGGTTTCAAGACATTTCTGACCGAGTGA 896
Qy 1337 AATTTTAGCGTGTATGTTGGATGCCGTGTGTCATGACCTCGACACAGGGGAACCAACAA 1396
Db 897 AATTTTAGCGTGTATGTTGGATGCCGTGTGTCATGACCTCGACACAGGGGAACCAACAA 956
Qy 1397 TGCCCTTCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGCAACTCTGCTACCTT 1456
Db 957 TGCCCTTCAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATGCAACTCTGCTACCTT 1016
Qy 1457 GGAGCATCACCATTTCAACACCGCGTGATGATCCTTCAAAAGTGAAGGTCAACATATCTT 1516
Db 1017 GGAGCATCACCATTTCAACACCGCGTGATGATCCTTCAAAAGTGAAGGTCAACATATCTT 1076
Qy 1517 TGCTAACTGTCTCCCAAGGAATATAGTGACCTTTATGACAGCTTTTGAAGCAGTCAATATT 1576
Db 1077 TGCTAACTGTCTCCCAAGGAATATAGTGACCTTTATGACAGCTTTTGAAGCAGTCAATATT 1136
Qy 1577 GGCAACAGCTCACGCTGTACTTTTGAGAGGAGAACTGAATTTCTTGAACCTTGCAGTAA 1636
Db 1137 GGCAACAGCTCACGCTGTACTTTTGAGAGGAGAACTGAATTTCTTGAACCTTGCAGTAA 1196
Qy 1637 AGGAGAATACCATTTGGAACATCAAAACCATCTCGTGATATTTTCGATCAATGTTTAATGAC 1696
Db 1197 AGGAGAATACCATTTGGAACATCAAAACCATCTCGTGATATTTTCGATCAATGTTTAATGAC 1256
Qy 1697 AGCCTGTGACCTTGAGGCCGTGACCAACCGTGGAGATCTCCAGACAGGTGGCAGAACT 1756
Db 1257 AGCCTGTGACCTTGAGGCCGTGACCAACCGTGGAGATCTCCAGACAGGTGGCAGAACT 1316
Qy 1757 TGTAAACAGTACGTTCTTCGAACAGGAGATTCGGGAGAGATTTAGAGCTCAAACTCACTCC 1816
Db 1317 TGTAAACAGTACGTTCTTCGAACAGGAGATTCGGGAGAGATTTAGAGCTCAAACTCACTCC 1376
Qy 1817 TTACAGCAATTTTTCATCGGAACCGGAGGATGAACCTGCCCTCGTTCGAACTGGAGTGGAT 1876
Db 1377 TTACAGCAATTTTTCATCGGAACCGGAGGATGAACCTGCCCTCGTTCGAACTGGAGTGGAT 1436
Qy 1877 TGATAGCATCTGCATGCCCTTTTGTATCAGGCACCTGGTGAAGGTCAACGTGAACCTGAAGCC 1936
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Db 1437 TGATAGCATCTGCATGCGCTTTGTATCAGGCACTGGTGAAGGTCAACGTGAAGCTGAAGCC 1496
QY 1937 GATGCTAGATTCAGTACAGCAAGTAAGTGGGAAGAGCTACACCAAAACGACT 1996
Db 1497 GATGCTAGATTCAGTACAGCAAGTAAGTGGGAAGAGCTACACCAAAACGACT 1556
QY 1997 GCTGCCCTCAACTGCTCATCTCTCCCTGCCAGTGTATGGTAGCAAGGAAGACAG 2056
Db 1557 GCTGCCCTCAACTGCTCATCTCTCCCTGCCAGTGTATGGTAGCAAGGAAGACAG 1616
QY 2057 GAACATAA 2063
Db 1617 GAACATAA 1623

RESULT 7

US-10-094-168B-4
; Sequence 4, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094,168B
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1982
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDEL0A2
US-10-094-168B-4

Query Match 50.3%; Score 1045.6; DB 9; Length 1982;
Best Local Similarity 99.6%; Pred. No. 7,le-315;
Matches 1048; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 557 ACCAGTGTGAAATTTACCAATCCTTTGAATTGATGTCCTCCCAAGTGCAGTGTGATGC 616
Db 123 ACAGTGTGAAATTTACCAATCCTTTGAATTGATGTCCTCCCAAGTGCAGTGTGATGC 182
QY 617 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCAGCTGGCTTAATAATAA 676
Db 183 TGAGAACAGTTTCAAGAAAGCATGGAGAAATCATCATCTCCAGCTGGCTTAATAATAA 242
QY 677 CAGATTGCTGAGCTGGTTGCTTCAACAGGCTTCCAGTGAACATCAGTATGCTACCA 736
Db 243 CAGATTGCTGAGCTGGTTGCTTCAACAGGCTTCCAGTGAACATCAGTATGCTACCA 302
QY 737 GGATCCGCGCTTTGATGAGAGGAGGACAGATATCTGTTTTCACATAAGATCTGTCT 796
Db 303 GGATCCGCGCTTTGATGAGAGGAGGACAGATATCTGTTTTCACATAAGATCTGTCT 362
QY 797 TTGTGCTCCTATTGGGAATACCAACCAATTAATTGGAGTGGCTCAAGTGTAAACAG 856
Db 363 TTGTGCTCCTATTGGGAATACCAACCAATTAATTGGAGTGGCTCAAGTGTAAACAG 422
QY 857 ACTTGATGGGAACCTTTTGTGATGAGATCAACAGCTTTTTCAGGCTTTTGTGATCTT 916
Db 423 ACTTGATGGGAACCTTTTGTGATGAGATCAACAGCTTTTTCAGGCTTTTGTGATCTT 482
QY 917 TTGTGAGCTTGGCATCAACACAAATATGATCAAGTGAAGAGTCTCTGGGCAA 976

Db 483 TTGTGAGCTTGGCATCAACAAACAAATATGATGATCAAGTGAAGAGTCTCTGGGCAA 542
QY 977 GCAGTCTGTGCTCTTGTATGCTATCATACCATCGACATGTTCAAAAGCTGAAGTTGA 1036
Db 543 GCAGTCTGTGCTCTTGTATGCTATCATACCATCGACATGTTCAAAAGCTGAAGTTGA 602
QY 1037 CAAGTTTAAAGCAGCAACATCCCTCTGCTGTGTCAGAACTTGCATCGATGACATTCATTT 1096
Db 603 CAAGTTTAAAGCAGCAACATCCCTCTGCTGTGTCAGAACTTGCATCGATGACATTCATTT 662
QY 1097 TGATGACTTTTCTCTCGACGTTGATGCGCATGATCAGCTGCTCTCCGGATGTTTCATGGA 1156
Db 663 TGATGACTTTTCTCTCGACGTTGATGCGCATGATCAGCTGCTCTCCGGATGTTTCATGGA 722
QY 1157 GCTGGGATGTTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 1216
Db 723 GCTGGGATGTTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGTGGCTTTTGAC 782
QY 1217 AGTGAGGAAAAATATCGGATGGTTCATACCAACTGGAGACATGCTTCAACGTGTG 1276
Db 783 AGTGAGGAAAAATATCGGATGGTTCATACCAACTGGAGACATGCTTCAACGTGTG 842
QY 1277 TCAGTGTATGTCGCGATGTTAAACACTGCTGGGTTTCAAGACATTCAGCCGAGGTGGA 1336
Db 843 TCAGTGTATGTCGCGATGTTAAACACTGCTGGGTTTCAAGACATTCAGCCGAGGTGGA 902
QY 1337 AATTTAGCGGTGATGTTGGGATGCCCTGTGTCATGACCTCGACACACAGGGGAACAA 1396
Db 903 AATTTAGCGGTGATGTTGGGATGCCCTGTGTCATGACCTCGACACACAGGGGAACAA 962
QY 1397 TGCCTTCCAAAGCTAAGAGTGGCTGCTGCCCTGGCCCAACTCTATGAACTCTGCTACCTT 1456
Db 963 TGCCTTCCAAAGCTAAGAGTGGCTGCTGCCCTGGCCCAACTCTATGAACTCTGCTACCTT 1022
QY 1457 GGAGCATCACATTTCAACACGCGGTGATGATCCTTCAAAAGTGAAGGTGAGGTGATATCTT 1516
Db 1023 GGAGCATCACATTTCAACACGCGGTGATGATCCTTCAAAAGTGAAGGTGAGGTGATATCTT 1082
QY 1517 TGCTAACCTGTCTCCCAAGGAATATAGTACCTTATGAGCTTTTGAGCAGTCAATATT 1576
Db 1083 TGCTAACCTGTCTCCCAAGGAATATAGTACCTTATGAGCTTTTGAGCAGTCAATATT 1142
QY 1577 GGCAACAGCTCACGCTGTACTTTTGAGGAGA 1608
Db 1143 GGCAACAGCTCACGCTGTACTTTTGAGGAGA 1174

RESULT 8

US-09-891-216-4
; Sequence 4, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973 00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-891-216-4

Query Match 18.7%; Score 388.8; DB 10; Length 426;

Best Local Similarity 99.5%; Pred. No. 1.6e-110;
Matches 390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 171 GATCGACGATTCATGATGAATCGACAAGCTGACTGGATACAGACAAAATCATTTG 230
Db 1 CATCGACGATTCATGATGAATCGAANGCTACTGGATACAGACAAAATCATTTG 60

QY 231 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTGGTGGCCCAAGCGATAAATAAG 290
Db 61 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTGGTGGCCCAAGCGATAAATAAG 120

QY 291 ATTCCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTCCA 350
Db 121 ATTCCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTCCA 180

QY 351 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 410
Db 181 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 240

QY 411 AGAAGCAGAGTTTGTCTAGAGTGGTTAATGACCTCTTTGAAGACACAGCTGACCTGGAG 470
Db 241 AGAAGCAGAGTTTGTCTAGAGTGGTTAATGACCTCTTTGAAGACACAGCTGACCTGGAG 300

QY 471 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGACGGCTGTCT 530
Db 301 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGACGGCTGTCT 360

QY 531 GTTTTACTCTTAGAGGACATCGAATCACCAGT 562
Db 361 GTTTTACTCTTAGAGGACATCGAATCACCAGT 392

RESULT 9
US-09-891-216-11
; Sequence 11, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-891-216-11

Query Match 18.7%; Score 388.8; DB 10; Length 426;
Best Local Similarity 99.5%; Pred. No. 1.6e-110;
Matches 390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 171 GATCGACGATTCATGATGAATCGACAAGCTGACTGGATACAGACAAAATCATTTG 230
Db 1 GATCGACGATTCATGATGAATCGACAAGCTAAGCTGATACAGACAAAATCATTTG 60

QY 231 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTGGTGGCCCAAGCGATAAATAAG 290
Db 61 TGCATGCTATCCGAAGCAGTGATGGTGAGATTATTGGTGGCCCAAGCGATAAATAAG 120

QY 291 ATTCCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTCCA 350
Db 121 ATTCCTGAAGAGCTCCATTTACTGAAGATGATGAAAAAGTTATGCAGATGTATCTCCA 180

QY 351 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 410
Db 181 TTTTGTGGAATCGCCATATCTAAGCTCAGCTCTTTTGTGCTCAAGGAAAAGATATGAA 240

QY 411 AGAAGCAGAGTTTGTCTAGAGTGGTTAATGACCTCTTTGAAGACACAGCTGACCTGGAG 470
Db 241 AGAAGCAGAGTTTGTCTAGAGTGGTTAATGACCTCTTTGAAGACACAGCTGACCTGGAG 300

QY 471 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGACGGCTGTCT 530
Db 301 AAAATTGTCAAGAAAATAATGCATCGGGCCCAAACTCTGCTGAAATGTGACGGCTGTCT 360

QY 531 GTTTTACTCTTAGAGGACATCGAATCACCAGT 562
Db 361 GTTTTACTCTTAGAGGACATCGAATCACCAGT 392

RESULT 10
US-10-115-515-22
; Sequence 22, Application US/10115515
; Publication No. US20030054992A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Corbin, Jackie D.
; Ferguson, Kenneth M.
; Francis, Sharron H.
; Kadlecik, Ann
; Loughney, Kate
; McAllister-Lucas, Linda M.
; Sonnenburg, William K.
; Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,515
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/599,658
; FILING DATE: 21-Jun-2000
; APPLICATION NUMBER: 09/055,584
; FILING DATE: 4-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030054992A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 12..2636

Db 1705 CTGTGGTACCATCTGCCAGACCCTTAAATCACTGACTTCAGCTTCAGCGACTTTTGAGC 1764
Qy 1111 TCAGAGTTGATGCCATGATCAGAGCTGCTCCGGATGTTTCATGAGCTGGGATGGTAC 1170
Db 1765 TGTCTGACCTGGAACAGCACTGTGCACAAATCCGGATGTTCACTGACCTCAACCTTTGTC 1824
Qy 1171 AGAAATTTAAATGACTATGAGACACTGTGTAGTGGCTTTTACAGTGAAGAAACT 1230
Db 1825 AGAATCTCCAGATGAACATGAGTCCCTTTTCAAGTGGATTTAAAGTGAAGAAACT 1884
Qy 1231 ATCGGATG--GTTCTATACCACACTGGAGACATGCTTCAAGCTGTGTGAGCTGATG 1287
Db 1885 ATCGGAGAAGCTCGCCTATCATTAATTTGGAGACATGCTTTAATACAGCTCAGTGCATGT 1944
Qy 1288 TCGGGATGTTAAACCACTGCTGGTTCGAAGACATTTCAAGGAGTGGGAAATTTAGCGG 1347
Db 1945 TTGGCGCACTAAACAGGCAAAATTCAGAGAGGCTGACGGACCTGGAGATACCTGCAC 2004
Qy 1348 TGATTTGGGATGCTGTGTCATGACCTCGACACAGGGGAACCAATGCCCTTCCAAAG 1407
Db 2005 TGCTGATTTGCTGCTTAAGCCATGATCTGGATCACCGTGGTGTCAATAAATCATACATAC 2064
Qy 1408 CTAAGAGTGGCTGCTGCTGCGCCCAACTCTATGGAACCTCTGCTACCTTGAGCATCAC 1467
Db 2065 AGCGAAGTGAACACCCACTTGTCTCAGCTCTACTG---CCATTCAATCATGAGCATCATC 2121
Qy 1468 ATTTCAACACCGCGTGTATGATCTTCAAGTGAAGGTGACAAATATCTTTGCTAAACCTGT 1527
Db 2122 ATTTGATCAGTGCCTGATGATCTTAATAGTCTGGCAATCAGATTCAGTGGCCTCT 2181
Qy 1528 CCTCCAAGGATATAGTACCTTATGACGCTTTTGAAGCAGTCAATATTTGCAACAGACC 1587
Db 2182 CCATTGAAGAGTATAAGACACCCCTGAAGATCATCAAGCAAGCTATTTTACCCACAGACC 2241
Qy 1588 TCAGCTCTACTTTGAGAGGAGAACTGAATCTTTTGAAGTGTGCTAGTAAAGAGAAATACG 1647
Db 2242 TAGCACTGTACATAAAGAGAGAGGAGAAATTTTGAACCTTATAATGAAATCAATTTCA 2301
Qy 1648 ATTTGAACATCAAAACCACTGCTGATATATTTGATCAATGTTAATGACAGCTGTGACC 1707
Db 2302 ATTTGGAAGATCCTCATCAAAAGAGTGTGTTTAGCGATGCTGATGACACTTTGTGATC 2361
Qy 1708 TTGGAGCGGTGACCAACCGTGGGAGATCTCCAGACAGGTGCGAGAACTTTGAACCAAGTG 1767
Db 2362 TTTCTGCAATTTACAAAACCGTGGCTTATTAACAACGGATAGCAGAACTTTGCGCACTG 2421
Qy 1768 AGTTCTTGAACAGGAGATCGGAGATAGAGCTCAAACTCACTCTCTCAGCAATTT 1827
Db 2422 AATTTTGGCAAGGAGATAGAGAGAGAAAGAACTCAACATAGAGCCGCTGATCTAA 2481
Qy 1828 TTGATCGGAACCGGAAGGATGAAGTGGCTGCAACTGAGTGGATTTGATAGCATCT 1887
Db 2482 TGAACGGGAGAGAAACAAATCCCAAGTATGCAAGTTGGATTCATAGATGCCATCT 2541
Qy 1888 GCATGCTTTTATCAGGCACTGTGAGAGTCAACGTGAAGTGAAGCTGAAGCCGATGCTAGAT 1947
Db 2542 GCTTGCACCTGATGAGCGCTTGACCCATGTGTGCGAGGACTGTTCCCTTTGCTGGACG 2601
Qy 1948 CAGTAGCTACAAACAGAGTAGTGGGAGAGCT 1981
Db 2602 CCTGAGAAAGAACAGGAGAGAAATGGCAGGCTCT 2635

RESULT 13

US-09-321-801-1
: Sequence 1, Application US/09321801
: Patent No. US20020115176A1
: GENERAL INFORMATION:
: APPLICANT: Lanfear, Jeremy
: APPLICANT: Robas, Nicola M.
: TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMS
: FILE REFERENCE: PC9477A
: CURRENT APPLICATION NUMBER: US/09/321.801

: CURRENT FILING DATE: 1999-05-27
: EARLIER APPLICATION NUMBER: 9826777.6
: EARLIER FILING DATE: 1998-12-04
: EARLIER APPLICATION NUMBER: 9823882.7
: EARLIER FILING DATE: 1998-10-30
: EARLIER APPLICATION NUMBER: 9811500.9
: EARLIER FILING DATE: 1998-05-28
: EARLIER APPLICATION NUMBER: 9908247.1
: EARLIER FILING DATE: 1998-04-09
: EARLIER APPLICATION NUMBER: 9910801.1
: EARLIER FILING DATE: 1999-05-10
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 2554
: TYPE: DNA
: ORGANISM: Human
US-09-321-801-1

Query Match 10.5%; Score 219.2; DB 10; Length 2554;
Best Local Similarity 50.8%; Pred. No. 4.7e-57;
Matches 667; Conservative 0; Mismatches 623; Indels 24; Gaps 5;

Qy 668 AATAAATAACAGCAATTCGTGAGCTGGTTCCTCAACAGGCCCTTCAGTGAACATCAGTGA 727
Db 1017 AATTGAGAAAGAAATTCGTGCCAAGTAGCAAGAACAGGGAAGTCTCTGAACATTTCCAGA 1076
Qy 728 TGCTTACCAGATCCGCGCTTTGATGACAGAGGACAGACAGATATCTGCTTTTCACATAG 787
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Qy 1088 CATTCAATTTTGTGACTTTTCTCTCGAGCTTGATGCCATGATCAGCTGCTCTCCGGAT 1147
Db 1425 AATTGAATTTTCCACTTTGACATTTGGCTTTTGAAGAACATGTCGCTGGAATTTTGT 1484
Qy 1148 GTTCATGAGCTGGGGATGGTACAGAAATTTAAATTTGACTATGACACACTGTGTAGCTG 1207
Db 1485 CTACATGGTTCATCGTCTCTGGGACATCTGCTTTGAGCTTGAAGAGTTGTGTCTGTT 1544
Qy 1208 GCTTTTTCAGCTGAGGAAAACTATCGGATGGTTCATACCAACTGGAGACATGCTCT 1267
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Qy 1268 CAACGTGTGCTGAGTGTTCGCGATGTTAACTGTTAACTGCTGCTGCTTCAAGACATTTCTAC 1327
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Qy 1328 CGAGGTGGAATTTTATAGCGGTGATTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1387
Db 1659 AGACCTTGAGCGCAAGGACTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1718
Qy 1388 AACCAACAATGCCCTTCCAAAGCTAAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447

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Qy 1568 GTCATATGTCACAGACCTCAGCTGTACTTTGAGAGGAACTGAATTTCTTTGAACT 1627
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Qy 1928 ACTGAAGCCGATGCTAGATTGAGTGTACAAACAGAGTAAGTGGGAGAGCT 1981
Db 2253 CACGAGGCTCTTCTGAAGCATGACAGGAGTAATCTCAGTCAGTGGGAGAGGT 2306

RESULT 14

US-09-321-801-3
; Sequence 3, Application US/09321801
; Patent No. US20020115176A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Robas, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477A
; CURRENT APPLICATION NUMBER: US/09/321.801
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 9826777.6
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 9823882.7
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 9811500.9
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 9908247.1
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 9910801.1
; EARLIER FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 2798
; TYPE: DNA
; ORGANISM: Human
US-09-321-801-3

Query Match 10.5%; Score 219.2; DB 10; Length 2798;
Best Local Similarity 50.8%; Pred. No. 5.1e-57;
Matches 667; Conservative 0; Mismatches 623; Indels 24; Gaps 5;
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Db 1439 GGTCAACAAAATCAGTGGCAGTGTCTCTCTAAAACAGATGAAAACAACCTTTCAAAATGTT 1498
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Qy 1148 GTTCATGAGCTGGGATGTTACAGAAATTTAAATTTGACTATGAGACACTGTGTAGGTG 1207
Db 1730 CTACATGTTTCATCGCTCTCTGGGACATCTCTGCTTGGAGCTTGAAGATTTGTCTGCTTT 1789
Qy 1208 GCTTTTGACATGAGGAAACATCTCGGATGGTTCTATACCAACTCGGAGACATGCCTTT 1267
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Qy 1328 CGAGGTGGAAATTTTAGCGGTGATTGTGGGATGCTGTGTCATGACCTCGACACAGGG 1387
Db 1904 AGACCTTGAGCGCAAGGAGCTGCTGATGCTGCTGTGTCATGACCTTGACACAGGG 1963
Qy 1388 AACCAACAATGCCCTTCCAAGCTAAGAGTGGCTCTGCGCTGGCCCAACTCTATGGAACCTC 1447
Db 1964 CTTCAAGTAACAGCTACCTGTCAGAAAGTTGCGACACCGCTCTGACCGCTCTCTAC---TCCAC 2020
Qy 1448 TGCTACCTTGGAGCATCACCATTTTCAACACCGCGTGATGATCTCTTCAAGTGAAGGTCA 1507
Db 2021 TTCCACCATGGAGCAGCAGCAGCTTCTCCGACGTGTGTCATCTCTAGTTGGAGGGCA 2080
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Qy 1928 ACTGAAGCCGATCTAGATTTCAGTAGCTACAAACAGAGTAAGTGGGAAGAGCT 1981
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RESULT 15
US-09-420-190-2
; Sequence 2, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 4381
; TYPE: DNA.
; ORGANISM: Homo sapiens.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(2403)
US-09-420-190-2

Query Match 10.5% Score 217.6; DB 10; Length 4381;
Best Local Similarity 50.7%; Pred. No. 2.2e-56;
Matches 666; Conservative 0; Mismatches 624; Indels 24; Gaps 5;

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Db 1041 AATTGAAAAGGAATTGCTGGCCAAAGTAGCAAGAACAGGGGAAGTCTCTGAACATCCAGA 1100
Qy 728 TGCCATACCAGGATCCGGCTTTGATGAGAGGAGGACACAGATATCTGGTTTTACATAAG 787
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Qy 788 ATCTGTTCTTTGTCTGCTCTTTTGGGAATAGCAACCAACCAATTAATTGGAGTGGCTCAAGT 847
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Qy 848 GTTAAACAGACTTTGATGGGAAACCTTTTGTATGATGACAGATCAACAGCTTTTTCAGGCTTT 907
Db 1218 GGTCAACAAAATCAGTGGCAGTGCTTCTCTAAAACAGACAGAAACAACTTCAAAATGTT 1277
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Db 1278 TGCCGCTCTTTGTGCTTTAGCCTTACACTGTGCTAATATGATCATAGAATTCGCCACTC 1337
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Db 1338 AGAGTGCAATTTACGGGTAACAGATGGAAAGCTGCTCTACCATAGCATTTGTACTTCAGA 1397
Qy 1028 TGAAGTTGACAAGTTTAAGGAGCAGCAACATCCCTCTGCTGTCAGAACTTGCCATCGATGA 1087
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Search completed: June 20, 2003, 21:13:13
Job time : 335 secs

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Db 2277 CACGGAGCCTTCTCTGAAAGCATGCGAGGATAATCTCAGTCAGTGGGAGAGGT 2330
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:44:04 ; Search time 45.1845 Seconds
(without alignments)
3119.127 Million cell updates/sec

Title: US-09-663-542-1

Perfect score: 3516

Sequence: 1 MLKQARRPLFRNVLSTQWK.....ASTASSSPASVMVAKEDRN 684

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3516	100.0	684	Q9GZY7	Q9GZY7 homo sapien
2	3354	95.4	988	Q96S76	Q96S76 homo sapien
3	3294.5	93.7	685	Q8VID7	Q8VID7 rattus norv
4	3250	92.4	934	Q9HCR9	Q9HCR9 homo sapien
5	3117.5	88.7	935	Q8VID6	Q8VID6 rattus norv
6	2970	84.5	576	Q9HB46	Q9HB46 homo sapien
7	2845.5	80.9	581	Q8VID8	Q8VID8 rattus norv
8	2541	72.3	490	Q9NY45	Q9NY45 homo sapien
9	1511.5	43.0	1284	Q9VJ79	Q9VJ79 drosophila
10	1478	42.0	1018	Q95TW8	Q95TW8 drosophila
11	1380.5	39.3	1232	Q9VFI9	Q9VFI9 drosophila
12	1054.5	30.0	861	Q91LZ01	Q91LZ01 mus musculu
13	1021	29.0	857	Q8UUY6	Q8UUY6 rana pipien
14	1019.5	28.0	861	Q8UUY5	Q8UUY5 rana pipien
15	1017	28.9	866	Q8UUY7	Q8UUY7 rana pipien
16	998	28.4	856	Q9MYV0	Q9MYV0 canis famli

ALIGNMENTS

RESULT 1

ID	Q9GZY7	PRELIMINARY;	PRT;	684 AA.
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DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
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GN	PDE11A3 OR HSPDE11A.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20524097; PubMed=11050148;			
RA	Hetman J.M., Robas N.M., Baxendale R., Fidock M., Phillips S.C.,			
RA	Soderling S.H., Beavo J.A.;			
RT	"Cloning and characterisation of two splice variants of human phosphodiesterase 11A.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTIS;			
RX	MEDLINE=20469516; PubMed=10906126;			
RA	Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;			
RT	"Isolation and Characterization of Two Novel Phosphodiesterase PDE11A Variants Showing Unique Structure and Tissue-specific Expression.";			
RL	J. Biol. Chem. 275:31469-31479(2000).			
DR	EMBL; AJ278682; CAC15567.1; -			
DR	EMBL; AB038041; BAB16372.1; -			
DR	InterPro; IPR003018; GAF.			
DR	InterPro; IPR003607; ME_Pplase_HDC.			
DR	InterPro; IPR002073; PDEase.			
DR	Pfam; PF01590; GAF; 2.			
DR	Pfam; PF00233; PDEase; 1.			
DR	PRINTS; PR00387; PDIESTERASE1.			
DR	SMART; SM00065; GAF; 2.			

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Q8R0D4 mus musculu
Q9NTV4 homo sapien
Q9HCP9 homo sapien
Q9ULW9 homo sapien
Q96076 ephydalia f
Q9WV11 mus musculu
Q9QYJ5 rattus norv
Q9QYJ6 rattus norv
Q9GQU6 trypanosoma
Q8WQX9 trypanosoma
Q97746 canis famli
Q9GTH9 trypanosoma
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Q8R078 mus musculu
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Q35470 rattus norv
Q9VKE9 drosophila
P94181 anabaena sp
Q8SXR0 drosophila
Q8VIE3 rattus norv


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Qy 357 AIDDIHFDGSLDVDMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNW 416
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Qy 417 RHAFNVCOLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFAQKSGSALAOL 476
Db 721 RHAFNVCOLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFAQKSGSALAOL 780
Qy 477 YGTSATLEHHFHNHAFVMIQSEGHNIIFANLSSKEYSDLMOLLKOSILATDITLYFERTE 536
Db 781 YGTSATLEHHFHNHAFVMIQSEGHNIIFANLSSKEYSDLMOLLKOSILATDITLYFERTE 840
Qy 537 FFELVSKGEYDWNINKNHRDIPRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEGGDRER 596
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Db 901 LELKLTSAIDFRNRKDELPRLOLEWIDSICMPLYQALVKVNVKLPMLDSVATNRSKWE 960
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Db 961 ELHQKRLLASTASSSSPASVMVAKEDRN 988

RESULT 3
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AC Q8VID7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A3.
GN RNPDE11A3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059361; BAB79628.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 685 AA; 78067 MW; 505E8748E9A6C21F CRC64;

Query Match
Best Local Similarity 93.7%; Score 3294.5; DB 11; Length 685;
Matches 644; Conservative 13; Mismatches 23; Indels 7; Gaps 2;

Qy 1 MLKQARRPLFRNVLSATQWKVKITRLVQISGASLAEKQKHQDFLIQRTKTKDRFRND 60
Db 1 MLKQARRFSPNRSATQWRKVGSTROGQISGAFLAERLKHQDFLTRMQTTRTKDRFRND 60
Qy 61 EIDLKTYGKTKSLCLMCPIRNSDGEIIGVAQAINKVPEGAPFTEDEKVMQWYLPFCGIAI 120
|||||
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Db 61 EIDLKTYGKTKSLCLMCPIRNSDGEIIGVAQAINKVPEGAPFTEDEKVMQWYLPFCGIAI 120
Qy 121 SNAOLFASRREYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCCERCSVLLLED 180
Db 121 SNAOLFASRREYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCCERCSVLLLED 180
Qy 181 IESPVVKFTKSFELMSPKCSADAENSPKESMEKSSYSDWLNNSIAELVASTGLPVNISD 240
Db 181 IESPVVKFTKSFELMSPKCSADAENSPKESMEKSSYSDWLNNSIAELVASTGLPVNISD 240
Qy 241 AYQDPRDAEADQISGHIIRSVLCVPTWNSNHQIIGVAQVNLRLDGGKPFDDADQRLPEAF 300
Db 241 AYQDPRDAEADQISGHIIRSVLCVPTWNSNHQIIGVAQVNLRLDGGKPFDDADQRLPEAF 300
Qy 301 VIFGGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLYSELAIDD 360
Db 301 VIFGGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLYSELAIDD 360
Qy 361 IHFDDFSLDVDMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNHAF 420
Db 361 IHFDDFSLDVDMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKKNYRMVLYHNHAF 420
Qy 421 NVCOLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFAQKSGSALAOLYCTS 480
Db 421 NVCOLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFAQKSGSALAOLYCTS 480
Qy 481 ATLEHHFHNHAFVMIQSEGHNIIFANLSSKEYSDLMOLLKOSILATDITLYFERTEFFEL 540
Db 481 ATLEHHFHNHAFVMIQSEGHNIIFANLSSKEYSDLMOLLKOSILATDITLYFERTEFFEL 540
Qy 541 VSKGEYDWNINKNHRDIPRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEGGDRERLEK 600
Db 541 VSKGAYDWSITSHRDVFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEGGDRERSELK 600
Qy 601 LTPSAIDFRNRKDELPRLOLEWIDSICMPLYQALVKVNVKLPMLDSVATNRSKWEELHQ 660
Db 601 LTPSAIDFRNRKDELPRLOLEWIDSICMPLYQALVKVNVKLPMLDSVATNRSKWEELHQ 660
Qy 661 KRLLASTA-----SSSSPASVMVAKEDR 683
Db 661 KRLOVSAASPVPSPSPSPA---VAGEDR 684

RESULT 4
Q9HCR9 ID Q9HCR9 PRELIMINARY; PRT; 934 AA.
AC Q9HCR9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A (Phosphodiesterase 11A4).
GN HSPDE11A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=20469516; PubMed=10906126;
RA Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
RT "Isolation and Characterization of Two Novel Phosphodiesterase PDE11A
Variants Showing Unique Structure and Tissue-specific Expression.";
RL J. Biol. Chem. 275:31459-31479(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB036704; BAB16371.1; -.
DR EMBL; AB048423; BAB62712.1; -.

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DR EMBL; AB048403; BAB62712.1; JOINED.
DR EMBL; AB048404; BAB62712.1; JOINED.
DR EMBL; AB048405; BAB62712.1; JOINED.
DR EMBL; AB048406; BAB62712.1; JOINED.
DR EMBL; AB048408; BAB62712.1; JOINED.
DR EMBL; AB048409; BAB62712.1; JOINED.
DR EMBL; AB048410; BAB62712.1; JOINED.
DR EMBL; AB048411; BAB62712.1; JOINED.
DR EMBL; AB048412; BAB62712.1; JOINED.
DR EMBL; AB048413; BAB62712.1; JOINED.
DR EMBL; AB048414; BAB62712.1; JOINED.
DR EMBL; AB048415; BAB62712.1; JOINED.
DR EMBL; AB048416; BAB62712.1; JOINED.
DR EMBL; AB048417; BAB62712.1; JOINED.
DR EMBL; AB048418; BAB62712.1; JOINED.
DR EMBL; AB048419; BAB62712.1; JOINED.
DR EMBL; AB048420; BAB62712.1; JOINED.
DR EMBL; AB048421; BAB62712.1; JOINED.
DR EMBL; AB048422; BAB62712.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 934 AA; 104810 MW; 994675824259447E CRC64;

Query Match      92.4%; Score 3250; DB 4; Length 934;
Best Local Similarity 99.8%; Pred. No. 3.4e-233;
Matches 630; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 54 KDRFNDEIDKLTGYKTKSLLCMPIRSDGELIIGVAQAINKIPGAPFTEDEKVMOMYL 113
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 QDRFNDEIDKLTGYKTKSLLCMPIRSDGELIIGVAQAINKIPGAPFTEDEKVMOMYL 363

QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKTMHRAQTLLKCERC 173
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKTMHRAQTLLKCERC 423

QY 174 SVLLEDIESPVVFKTSFELMSPKCSADAENSKESKSSYSDWLINNSIAELVASTG 233
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
424 SVLLEDIESPVVFKTSFELMSPKCSADAENSKESKSSYSDWLINNSIAELVASTG 483

QY 234 LPVNISDAYODPRDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDCKPFDAD 293
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
484 LPVNISDAYODPRDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDCKPFDAD 543

QY 294 QRLFEAFVIFCGLGINNTIMYDQVKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLV 353
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
544 QRLFEAFVIFCGLGINNTIMYDQVKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLV 603

QY 354 SELAIDDIHFDDFSLVDAMITAAALRMFMELGMVQVKFKIDYETLCRWLLTVRKNYRMVLY 413
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
604 SELAIDDIHFDDFSLVDAMITAAALRMFMELGMVQVKFKIDYETLCRWLLTVRKNYRMVLY 663

QY 414 HNRHAFNVQCLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSAL 473
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
564 HNRHAFNVQCLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSAL 723

QY 474 AOLYGTSATLEHHFHNHAFVILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYFER 533
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 AOLYGTSATLEHHFHNHAFVILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYFER 783

QY 534 RTEFFELVSGEYDWNKTHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFPQGD 593
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
784 RTEFFELVSGEYDWNKTHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFPQGD 843

QY 594 RERLELKTPTSAIFDRNRKDELPRLOLEWIDSCIMPLYQALVKNVKNLKPMLDSVATNRS 653
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
844 RERLELKTPTSAIFDRNRKDELPRLOLEWIDSCIMPLYQALVKNVKNLKPMLDSVATNRS 903

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QY 654 KWEELHOKRLLASTASSSSPASVVMVAKEDRN 684
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
904 KWEELHOKRLLASTASSSSPASVVMVAKEDRN 934

RESULT 5
Q8VID6
ID Q8VID6 PRELIMINARY; PRT; 935 AA.
AC Q8VID6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A4..
GN RNPDE11A4
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059362; BAB79629.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 935 AA; 104570 MW; E80F1039770F8276 CRC64;

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Query Match      88.7%; Score 3117.5; DB 11; Length 935;
Best Local Similarity 95.6%; Pred. No. 2.5e-223;
Matches 606; Conservative 9; Mismatches 12; Indels 7; Gaps 2;

QY 54 KDRFNDEIDKLTGYKTKSLLCMPIRSDGELIIGVAQAINKIPGAPFTEDEKVMOMYL 113
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 QDRFNDEIDKLTGYKTKSLLCMPIRSDGELIIGVAQAINKIPGAPFTEDEKVMOMYL 363

QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKTMHRAQTLLKCERC 173
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKTMHRAQTLLKCERC 423

QY 174 SVLLEDIESPVVFKTSFELMSPKCSADAENSKESKSSYSDWLINNSIAELVASTG 233
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
424 SVLLEDIESPVVFKTSFELMSPKCSADAENSKESKSSYSDWLINNSIAELVASTG 483

QY 234 LPVNISDAYODPRDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDCKPFDAD 293
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
484 LPVNISDAYODPRDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDCKPFDAD 543

QY 294 QRLFEAFVIFCGLGINNTIMYDQVKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLV 353
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
544 QRLFEAFVIFCGLGINNTIMYDQVKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLV 603

QY 354 SELAIDDIHFDDFSLVDAMITAAALRMFMELGMVQVKFKIDYETLCRWLLTVRKNYRMVLY 413
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
604 SELAIDDIHFDDFSLVDAMITAAALRMFMELGMVQVKFKIDYETLCRWLLTVRKNYRMVLY 663

QY 414 HNRHAFNVQCLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSAL 473
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
664 HNRHAFNVQCLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFQAKSGSAL 723

QY 474 AOLYGTSATLEHHFHNHAFVILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYFER 533
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 AOLYGTSATLEHHFHNHAFVILQSEGHNIIFANLSSKEYSDLMQLLKOSILATDLTYFER 783

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QY 534 RTEFFELVSKGEYDWNINKNHRDIFRSMMLTACDLGAVTKPWEISQVAELVTSEFFEOGD 593
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
784 RTEFFELVSKGAYDWSITSHRDVFRSMMLTACDLGAVTKPWEISQVAELVTSEFFEOGD 843
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
QY 594 RERLEKLTPTSAIDFRNRKDELPRQLQLEWIDSICMPLYQALVKNVKKPMLDSVATNRS 653
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 844 RERSELKLTPTSAIDFRNRKDELPRQLQLEWIDSICMPLYQALVKNVKNVNAKLPMLDSVAANRR 903
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 654 KWHEELHOKRLLASTA----SSSSPASVVMVAKEDR 683
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 904 KWHEELHOKRLQVSAASPVPSPSPA---VAGEDR 934
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 6
Q9HB46 PRELIMINARY; PRT; 576 AA.
AC Q9HB46;
DB 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DE CAMP/CGMP phosphodiesterase 11A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=20524097; PubMed=11050148;
RA Hetman J.M., Robas N., Baxendale R., Fidock M., Phillips S.C.,
RA Soderling S.H., Beavo J.A.;
RT "Cloning and characterization of two splice variants of human
RT phosphodiesterase 11A.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).
DR EMBL; AF281865; AAG32023.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 576 AA; 65766 MW; 3992C4C95A5B0B36 CRC64;

Query Match 84.5%; Score 2970; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.2e-212;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MMYLPPCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTL 168
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 1 MMYLPPCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTL 60
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 169 KCERCSVLLLEDIESPVVKFTKSFELMSPKCSADAENSKFESMEKSSYSDWLINNSIAEL 228
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 61 KCERCSVLLLEDIESPVVKFTKSFELMSPKCSADAENSKFESMEKSSYSDWLINNSIAEL 120
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 229 VASTGLPWNISDAYQDPRFDEADQISGFHRSVLCVPINWNSHQIIGVAQVNLNLDGKP 288
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 121 VASTGLPWNISDAYQDPRFDEADQISGFHRSVLCVPINWNSHQIIGVAQVNLNLDGKP 180
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 289 FDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVLVDVLSVHATCSAEVDKPKAA 348
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 181 FDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVLVDVLSVHATCSAEVDKPKAA 240
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 349 NIPLYSELAIDDIHFDDFSLVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNY 408
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 241 NIPLYSELAIDDIHFDDFSLVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNY 300
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 409 RMVLYHNHRHAFNVQCLMFAMLTAGFQDILTEVEILAVIVGCLCHDLHGRGTNNAFQAK 468
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
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DB 301 RMVLYHNHRHAFNVQCLMFAMLTAGFQDILTEVEILAVIVGCLCHDLHGRGTNNAFQAK 360
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
QY 469 SCSALAOQYGTSAITLEHHHFHNAVMILOSEGHNIFANLSKEYSDMLMOLLKOSILATDIT 528
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 361 SCSALAOQYGTSAITLEHHHFHNAVMILOSEGHNIFANLSKEYSDMLMOLLKOSILATDIT 420
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
QY 529 LYFERRTTEFFELVSKGEYDWNINKNHRDIFRSMMLTACDLGAVTKPWEISQVAELVTSEF 588
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 421 LYFERRTTEFFELVSKGEYDWNINKNHRDIFRSMMLTACDLGAVTKPWEISQVAELVTSEF 480
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
QY 589 FEQGDRELERLEKLTPTSAIDFRNRKDELPRQLQLEWIDSICMPLYQALVKNVKKPMLDSV 648
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 481 FEQGDRELERLEKLTPTSAIDFRNRKDELPRQLQLEWIDSICMPLYQALVKNVKKPMLDSV 540
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
QY 649 ATNRSKWHEELHOKRLLASTASSSSPASVVMVAKEDRN 684
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 541 ATNRSKWHEELHOKRLLASTASSSSPASVVMVAKEDRN 576
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

RESULT 7
Q9VID8 PRELIMINARY; PRT; 581 AA.
AC Q9VID8;
DB 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DE Phosphodiesterase 11A2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
RT (PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059360; BAB79627.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 581 AA; 66141 MW; 2CA7C2F5DDB37D00 CRC64;

Query Match 80.9%; Score 2845.5; DB 11; Length 581;
Best Local Similarity 95.7%; Pred. No. 2.2e-203;
Matches 555; Conservative 6; Mismatches 12; Indels 7; Gaps 2;

QY 108 VMOMYLPFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTL 167
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 4 VMOMYLPFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTL 63
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 168 LKERCSCVLLLEDIESPVVKFTKSFELMSPKCSADAENSKFESMEKSSYSDWLINNSIAE 227
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 64 LKERCSCVLLLEDIESPVVKFTKSFELMSPKCSADAENSKFESMEKSSYSDWLINNSIAE 123
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 228 LVASTGLPWNISDAYQDPRFDEADQISGFHRSVLCVPINWNSHQIIGVAQVNLNLDGK 287
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 124 LVASTGLPWNISDAYQDPRFDEADQISGFHRSVLCVPINWNSHQIIGVAQVNLNLDGK 183
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 288 FDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVLVDVLSVHATCSAEVDKPKA 347
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
DB 184 FDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVLVDVLSVHATCSAEVDKPKA 243
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

QY 348 ANIPLYSELAIDDIHFDDFSLVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKN 407
|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
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Db 244 ANIPLVSELAIDDDHFDFFSLDVLVDAMITAAALRMFMELGMWQKFKIDYETLCRWLLTVRKN 303
QY 408 YRMVLYHNHRHAFNVQMLFAMLTAGFQDILTEVEILAVIGCLCHDHRGTNNAFQA 467
|||||
Db 304 YRMVLYHNHRHAFNVQMLFAMLTAGFQDILTEVEILAVIGCLCHDHRGTNNAFQA 363
|||||
QY 468 KGSALAOLYQTSATLEHHHFNHVMILQSGHNIFANLSSKEYSDMLQMLKQSLATDL 527
|||||
Db 364 KDSALAOLYQTSATLEHHHFNHVMILQSGHNIFANLSSKEYSDMLQMLKQSLATDL 423
|||||
QY 528 TLYFERRTEFFELYSKGEYDHNKHNHRDIFRSLMTACDLGAVTKPWEISQVAELVTSE 587
|||||
Db 424 TLYFERRTEFFELYSKGEYDHNKHNHRDIFRSLMTACDLGAVTKPWEISQVAELVTSE 483
|||||
QY 588 FFEQDRLRLKLTPTSAIFDRNRKDELPRQLQLEWIDSICMPLYQALVKVNVKPKMLDS 647
|||||
Db 484 FFEQDRLRLKLTPTSAIFDRNRKDELPRQLQLEWIDSICMPLYQALVKVNVKPKMLDS 543
|||||
QY 648 VATNRKWEELHQRKLLASTA-----SSSPASVMVAKEDR 683
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Db 544 VAANRRKWEELHQRKLLASTA-----SSSPASVMVAKEDR 580
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RESULT 8

Q9NV45
ID Q9NV45 PRELIMINARY: PRT: 490 AA.
AC Q9NV45;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 11A1.
GN PDE11A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKETAL MUSCLE;
RX MEDLINE=20202699; PubMed=10725373;
RA Fawcett L., Baxendale R., Stacey P., McGrouther C., Harrow I.,
Soderling S., Hewman J., Beavo J.A., Phillips S.C.;
RT "Molecular cloning and characterization of a distinct human
phosphodiesterase gene family:PDE11A.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:3702-3707(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AJ251509; CAB82573.1; -;
DR EMBL; AB048423; BAB62714.1; -;
DR EMBL; AB048408; BAB62714.1; JOINED.
DR EMBL; AB048409; BAB62714.1; JOINED.
DR EMBL; AB048410; BAB62714.1; JOINED.
DR EMBL; AB048411; BAB62714.1; JOINED.
DR EMBL; AB048412; BAB62714.1; JOINED.
DR EMBL; AB048413; BAB62714.1; JOINED.
DR EMBL; AB048414; BAB62714.1; JOINED.
DR EMBL; AB048415; BAB62714.1; JOINED.
DR EMBL; AB048416; BAB62714.1; JOINED.
DR EMBL; AB048417; BAB62714.1; JOINED.
DR EMBL; AB048418; BAB62714.1; JOINED.
DR EMBL; AB048419; BAB62714.1; JOINED.
DR EMBL; AB048420; BAB62714.1; JOINED.
DR EMBL; AB048421; BAB62714.1; JOINED.
DR EMBL; AB048422; BAB62714.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_Hdc.
DR InterPro; IPR002073; PDEase.
PFam; PF01590; GAF; 1.

DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDISTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_1; 1.
SQ SEQUENCE 490 AA; 55786 MW; 28FD77BC040834F4 CRC64;
Query Match 72.3%; Score 2541; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 8, 1e-181;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 195 MSPKCSADAENSPKESMEKSSYSDWLNINNSTAEVLASTGLPVNISDAYQDPRFPAEADQI 254
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Db 1 MSPKCSADAENSPKESMEKSSYSDWLNINNSTAEVLASTGLPVNISDAYQDPRFPAEADQI 60
|||||
Qy 255 SGFHRSVLCVPIWNSNHQIIGVAQVNLNRDLGKPFDDADQRLFEAFVIFCGLGINNTIMY 314
|||||
Db 61 SGFHRSVLCVPIWNSNHQIIGVAQVNLNRDLGKPFDDADQRLFEAFVIFCGLGINNTIMY 120
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Qy 315 DQVKKSWAKOSVALDVLISYHATCSKAEDKFKAAANIPLVSELAIDDDHFDFFSLDVLVDAMI 374
|||||
Db 121 DQVKKSWAKOSVALDVLISYHATCSKAEDKFKAAANIPLVSELAIDDDHFDFFSLDVLVDAMI 180
|||||
Qy 375 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQMLFAMLTAG 434
|||||
Db 181 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQMLFAMLTAG 240
|||||
Qy 435 FQDILTEVEILAVIGCLCHDHRGTNNAFQAQSGSALAOLYQTSATLEHHHFNHVM 494
|||||
Db 241 FQDILTEVEILAVIGCLCHDHRGTNNAFQAQSGSALAOLYQTSATLEHHHFNHVM 300
|||||
Qy 495 LQSEGHNIFANLSSKEYSDMLQMLKQSLATDLTYFERRTEFFELYSKGEYDWNKHNHR 554
|||||
Db 301 LQSEGHNIFANLSSKEYSDMLQMLKQSLATDLTYFERRTEFFELYSKGEYDWNKHNHR 360
|||||
Qy 555 DIFRSMMLTACDLGAVTKPWEISQVAELVTSEFFEQDRLRLKLTPTSAIFDRNRKDE 614
|||||
Db 361 DIFRSMMLTACDLGAVTKPWEISQVAELVTSEFFEQDRLRLKLTPTSAIFDRNRKDE 420
|||||
Qy 615 LPRLOLEWIDSICMPLYQALVKVNVKPKMLDSVATNRKWEELHQRKLLASTASSSPA 674
|||||
Db 421 LPRLOLEWIDSICMPLYQALVKVNVKPKMLDSVATNRKWEELHQRKLLASTASSSPA 480
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Qy 675 SVMVAKEDRN 684
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Db 481 SVMVAKEDRN 490
|||||

RESULT 9

Q9VJ79
ID Q9VJ79 PRELIMINARY: PRT: 1284 AA.
AC Q9VJ79;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE CG10231 protein.
GN CG10231.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foster C., Garg N.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Skupski M.P., Smith T.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
DR EMBL; AE003659; AAF53675.1; -.
DR FlyBase; FBgn0032686; CG10231.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
DR SEQUENCE 1284 AA; 141726 MW; F6873C90A9953430 CRC64;
Query Match 43.0%; Score 1511.5; DB 5; Length 1284;
Best Local Similarity 44.4%; Pred. No. 1.4e-103;
Matches 303; Conservative 126; Mismatches 202; Indels 51; Gaps 6;
QY 20 KKKVTRILVQISGASLAKEQKHQDFLIQRT-----KTKDRFRNDEI 62
Db 263 KKCLVSKLFCVCPRTVEEMEQDQEVVRVAVGTVAGHVAESGEPVNPIDAYODERFNCI 322
QY 63 DKLTGYKTKSLICMPIRSDDGEIIGVAQAINKIPGAFTEDEKVMQVLPFCGIAISN 122
Db 323 DSLTYGRTKALLCMPIKDSSGVIGVAQVINKM-NGECFSEIDERVFSSYLOFCGIGLRN 381
QY 123 AOLFAASKEYERSRALLVENVNDLEETDLEKIVKIMHRAQITLLKRCRCSVLLLEDE 182
Db 382 AOLYKESQLEIKRNQVLDLARMIFEOSTIEHVMFRILTHMQSLQCORVOILLVHEAD 441
QY 183 SPVVKFTSKSFELMSPKCSADAENSPKESMEKSSYSDWLINNSIAELVASTGLPVNISDAY 242
Db 442 KG--SFSRVDFEANDLSEEEATSRTPVE-----SRFPINIGITGHVATTGTVNPNAY 495
QY 243 QDPREDAAQDISGFIHRSVLCVPTWNSHQIIGVAQVNLNRDQKPFDDADQRLFEAFVI 302
Db 496 EDDREDASVDENSCFKHSILCMAIKNSLGQIIGVITQLINKFNELDFTKNDENFVEAFI 555
QY 303 FCGLGINTIMYDOYKKWAKOSVALDVLVSYHATCSKAEDVKF----- 345
Db 556 FCGMGLHNTHYKEAIVAKOSVTLVLSYHASATMDAHLRKOKOQOQAVGLRQAPL 615
QY 346 -----KAANIPLVSELAIDDIHFDDFSLDQVAMITAALRMFMELCMQVKFKIDYET 396

Db 616 SLPPRKKLQRLRLRPSAVHFLHDFKFDIFHEDDDTLKACLRMFLDLDFVERPHIDYEV 675
QY 397 LCRWLLTVRKNYRMVLYHNHRHAFNVQCMFAMLTITAGFQDILLTEVEILAVIVGCLCHDL 456
Db 676 LCRWLLSVKKKNRVNVTYHNHRHAFNVQCMFAMLTITAGFQDILLTEVEILAVIVGCLCHDL 735
QY 457 DHRGTNNAFAQKSGSALQLYGTSATLEHHHFNHVAVMILQSGHNTFANLSKEYSDLMQ 516
Db 736 DHRGTNNSFOIKASSPLAQLYSTS-TMEHHHFDQCLMILNSPGNOLANLSSDDYCRVIR 794
QY 517 LKQSIILATDLYPERTEFEFELVSKGEYDNWIKNHRDIFRSMMLTACDGLGAVTKPWEI 576
Db 795 VLEDAILSTDLAVYFKRGPFLSVSQPTSYWVAEPEPRALLRAMSMTVCDLSAITKPWEI 854
QY 577 SRQVAELVTSFEFEGQDRERLEKLTTPSAIFDRNRKDELPLQLEWIDSICMPLVCAALVK 636
Db 855 EKKRVADLVSSSEFEGQDMKEQELNITPIDIMNRKEDELPMQVNFIDSICLPIYEAFAT 914
QY 637 NVNKLKPLMDSVATNRKWEEL 658
Db 915 LSKLEPLVEGVDRNDRGHIDL 936
RESULT 10
Q95TW8
ID Q95TW8 PRELIMINARY; PRT; 1018 AA.
AC Q95TW8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE GH27433p.
GN CG8279.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Muscomorpha;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY058470; AAL13699.1; -.
DR FlyBase; FBgn0038237; CG8279.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
DR SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;
Query Match 42.0%; Score 1478; DB 5; Length 1018;
Best Local Similarity 45.7%; Pred. No. 3.1e-101;
Matches 305; Conservative 106; Mismatches 208; Indels 48; Gaps 8;
QY 28 VOISGASLAKEQKHQDFLIQRTKDRFRNDEIDKLTGYKTKSLICMPIRSDDGEIIG 87
Db 213 IGIAGVWATKO-----MINIKAYKDAKFNCIEDIKLTGYKTNALICMPICNYGDIIG 266
QY 88 VQAQINKTPEGAPFTEDDEKVMQVLPFCGIAISNAQLFAASRKEYERSRALLVENVNDF 147
Db 267 VQAQINKTNGCMFEDEHDEHVEIFRRLYTCGIGIQNAQLFEMSQVQVRRNQILLNARSIF 326
QY 148 EQSDTLEKIVKIMHRAQITLLKRCRCSVLLLE-----DIESP-----VVKFK 190
Db 327 EBONNLECLVTIKMTEARELLKRCRCSVFLVDCCAEASHLEKIIIEKPNQPATRAIKSD 386

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QY 191 SPE-----LMSPKCSADAENSFKESMEKSSYSDWLNINNSTIAELVASTGLPVDNSD 240
RA      |||      |      |      |      |      |      |      |      |      |
RA      |      |      |      |      |      |      |      |      |      |
Db 387 SFEKKMRNRTVLELGEVQAANNVSRPSVSELSSSTLA---QIAQFVATTGQTVNCD 443
RA      |      |      |      |      |      |      |      |      |      |
RA      |      |      |      |      |      |      |      |      |      |
QY 241 A-----YODPRFDAEADQISGFHRSVLCVPINWNSHQIIGVAQVLRDLGKPPDDAQD 294
RA      |      |      |      |      |      |      |      |      |      |
Db 444 VIEWVRDHNQIRAEDEIDS-----TQAILCMPINNAQKKVIGVAQLINKANGVPTDSDA 498
RA      |      |      |      |      |      |      |      |      |      |
QY 295 RLFEAFVIFCGLGINNTIMYDOVKKSWAKQSVLVDLSYHATCSKAEDYDKFAANIPLVS 354
RA      |      |      |      |      |      |      |      |      |      |
Db 499 SIFEAFVIFCGLGINHTQMYENACKLMAKQKVALECLSYHATASQDQTEKLTQDVIAEAE 558
RA      |      |      |      |      |      |      |      |      |      |
QY 355 ELAIDDIHDFDPSLDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVKRNRMVLYH 414
RA      |      |      |      |      |      |      |      |      |      |
Db 559 SYNLSYFTTFDELVDVDDTCRAVLRFMFQCNLYSOFQIPYDVLRCRWLVSRKNYRPVKYH 618
RA      |      |      |      |      |      |      |      |      |      |
QY 415 NWRHAFNVQCLMFAMLTAGFODILTEVEILAVIVGCLDHLDRGTNNAFQAKSGSALA 474
RA      |      |      |      |      |      |      |      |      |      |
Db 619 NWRHALNVAQTMFAMLTGKMERFMTDLEILGLLVACLCHDLDRGTNNAFQTKTESPLA 678
RA      |      |      |      |      |      |      |      |      |      |
QY 475 QLYGTSATLEHHHFNHAYMILQSEGNHIFANLSKEYSDLMQLLKQSLATDLYFFER 534
RA      |      |      |      |      |      |      |      |      |      |
Db 679 ILY-TTSMHEHHFDQCVMLNSELGNHIFQALSPEDYSVMKTVESAILSTDLMAYFKKR 737
RA      |      |      |      |      |      |      |      |      |      |
QY 535 TEFFELVSKGEYDMKKNHRDIFRSMMLTACDLGAVTRPWEISROVAELVTSEFFEQGD 594
RA      |      |      |      |      |      |      |      |      |      |
Db 738 NAFLELVENGDFDQGEKKDLCCGMMTACDVSAIAKPEWQHVQKVAKLVADEFFDQGL 797
RA      |      |      |      |      |      |      |      |      |      |
QY 595 ERLEKLTPSAIFDRNRKDELPRLOLEWIDSICMPLYQALVKNVYKLPMLDSVATNRSK 654
RA      |      |      |      |      |      |      |      |      |      |
Db 798 EKLQLOTPVAMMDREKDELPMQGVFDIVCLPLRYVLCDTFPWTITPLVEGTLENRRN 857
RA      |      |      |      |      |      |      |      |      |      |
QY 655 WELHOK 661
RA      |      |      |      |      |      |      |      |      |      |
Db 858 WODLAEK 864
RA      |      |      |      |      |      |      |      |      |      |

RESULT 11
Q9VF19 PRELIMINARY; PRT: 1232 AA.
ID Q9VF19
AC Q9VF19;
DT 01-MAR-2000 (TremBLrel. 13, Created)
DT 01-MAY-2001 (TremBLrel. 16, Last sequence update)
DE CG8279 protein.
GN CG8279.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Stadler A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003705; AAF55066.2;
DR Flybase: FBgn0038237; CG8279.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; ME_Pplase_HDC.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF01590; GAF; 2.
DR Pfam: PF00233; PDEase; 1.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00065; GAF; 2.
DR SMART: SM00471; HGC; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
DR PROSITE: PS00294; PRENYLIATION; UNKNOWN_1.
SQ SEQUENCE 1232 AA; 137426 MW; ECF6B9C3A71BAF74 CRC64;

Query Match 39.3%; Score 1380.5; DB 5; Length 1232;
Best Local Similarity 38.9%; Pred. No. 7.3e-94;
Matches 299; Conservative 109; Mismatches 211; Indels 149; Gaps 10;

QY 28 VOISGASLAERKQKHQDFLQRYKTKDRRREDEIDKLTGYTKSLCLMCPTRSDGEIIG 87
Db      |      |      |      |      |      |      |      |      |      |
Db 326 IGIAGWVAQTKQ-----MINIKEAYKADARENCEIDLTKYKTNAILCMPCINVEGDIIG 379
QY 88 VQAQAIKPIEGAPFTEDDEKVMQYLPFCGTAISNAQLFAASRKEYERSALLVNDLF 147
Db      |      |      |      |      |      |      |      |      |      |
Db 380 VQAIIKNTGNCMEFDEHDEVEIFRRYLTFCGIGIQNAQLFEMSVQRYRNRQILLNARSIF 439
QY 148 EEQTDLEKIVKIMHRAQTLTKCERCVSLLLE-----DIESP-----VVKFTK 190
Db      |      |      |      |      |      |      |      |      |      |
Db 440 EEQNLECLVTKIMTEARELLKRCRCSVFLVDLDCCEASHLEKIEKPNQPATRAIKSAD 499
QY 191 SFE-----LMSPKCSADAENSFKESMEKSSYSDWLNINNSTIAELVASTGLPVDNSD 240
Db      |      |      |      |      |      |      |      |      |      |
Db 500 SFEKKMRNRTVLELGEVQAANNVSRPSVSELSSSTLA---QIAQFVATTGQTVNCD 556
QY 241 A-----YODPRFDAEADQISGFHRSVLCVPINWNSHQIIGVAQVLRDLGKPPDDAQD 294
Db      |      |      |      |      |      |      |      |      |      |
Db 557 VIEWVRDHNQIRAEDEIDS-----TQAILCMPINNAQKKVIGVAQLINKANGVPTDSDA 611
QY 295 RLFEAFVIFCGLGINNTIMYDOVKKSWAKQSVLVDLSYHATCSKAEDYDKFAANIPLVS 354
Db      |      |      |      |      |      |      |      |      |      |
Db 612 SIFEAFVIFCGLGINHTQMYENACKLMAKQKVALECLSYHATASQDQTEKLTQDVIAEAE 671
QY 355 ELAIDDIHDFDPSLDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVKRNRMVLYH 414
Db      |      |      |      |      |      |      |      |      |      |
Db 672 SYNLSYFTTFDELVDVDDTCRAVLRFMFQCNLYSOFQIPYDVLRCRWLVSRKNYRPVKYH 731
QY 415 NWRHAFNVQCLMFAMLTAGFODILTEVEILAVIVGCLDHLDRGTNNAFQAKSGSALA 474
Db      |      |      |      |      |      |      |      |      |      |
Db 732 NWRHALNVAQTMFAMLTGKMERFMTDLEILGLLVACLCHDLDRGTNNAFQTKTESPLA 791
QY 475 QLYGTSATLEHHHFNH-----
Db      |      |      |      |      |      |      |      |      |      |
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Db 792 ILY-TTSMHHFDFHFLAAFLDRLAARRALRDRLARELLDLVBEELVVDPTLIELVIEY 850
QY 491 -----AVMLIQS----- 497
Db 851 FLLRLRTFLPEPELDEDDDDVDSVVSVLVLDLSVLVLSAALTWATYKTTIER 910
QY 498 -----EGHNIFANLSSKEYSDLMQLLKQSILATDLYFERTEFFELYSKGEYDWNKIH 553
Db 911 TKTRDRNEMLDALSPEDYSVMKTVESAILSTDLMAYEKKRNFALVELVEGEFDQGEK 970
QY 554 RDIFRSMLMTACDLGAVTKPWEISQVAELVTSFEFGDRRLBLKTPPSAIFDRNRKD 613
Db 971 KDLICGMNMTACDVSAAIPKPEVQHAKVLVADEEFDQGLKQLNTQPVAMMDRERKD 1030
QY 614 ELPRLOLEWIDICMPLVQALVKNVVKLPMKLDVATNRKSWHEELHOK 661
Db 1031 ELPKMQVGFIDVLCPLRVLCDTFPWITPLYEGTLENRRNQDLAEK 1078

RESULT 12
Q912Q1
ID Q912Q1 PRELIMINARY; PRT; 861 AA.
AC Q912Q1
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE CGMP phosphodiesterase 6c.
GN PDE6C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=RETINA;
RA Chang B., Hawes N.L., Hurd R.E., Davisson M.T., Nusinowitz S.,
RA Heckenlively J.R.;
RT "A sequence alteration in pde6c gene causes cone photoreceptor
RT function loss (cpfl1) in mice.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411063; AAK96254.1; -.
DR MGD; MGI:105936; Pde6c.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 861 AA; 98785 MW; C582D78114652B5B CRC64;

Query Match 30.0%; Score 1054.5; DB 11; Length 861;
Best Local Similarity 35.5%; Pred. No. 8.1e-70;
Matches 243; Conservative 130; Mismatches 242; Indels 69; Gaps 16;

QY 54 KORFENDEIDKTYKTKSLCMLPSSDGEIIGVAAQAINKIPEGAP-FTEDEKVMQMY 112
Db 160 KNSHESDFMDKQTGYVTRNLLAVPIVAGK-EVLAVVMVANKI--SAPEFSKODEEVFSKY 216
QY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCR 172
Db 217 LSFVAVALRQHTSVLYSVESRRSQILMWSANKVFEEITDVERQHKALYTIIRTINCDR 276
QY 173 CSVLLL-----EDIESPVVKTKSFELMSPKCSADAENSF-----KESME--KS 214
Db 277 YSIGLLDMTKKEFYDEWPKLGEVPEYKGPRTDGPRTIIFYKIIDIYILHGKEEINVPIS 336
QY 215 SYSD-WLINNSIAELVASTGLPVNTSDAYODPRFEADAQI--SGFHRSVLCVPTWNSN 271
Db 337 PRADHWTLVSGLPTVAENGFTCNMLNAPADEYFFQKGPVDTEGWIKNVLSLPLVKK 396
QY 272 HQIIGVAQVNLRLDGKPFDDADQRLFEAFVIFCGLGINNNTIMYDQVKKSWAKQSVALDVL 331
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Db 397 EDIVGVATFYNRKDGKPFDEHDEHITETLTQGLWSLLNTDTYERVNKLESKDKIAQEMV 456
QY 332 SVHATCSRAEVD---KFK-AANIPLVSE-----LAI-----DDIH---FDDFSL 368
Db 457 MNLTKATPEDEISSILKFKKLNVEIECEERQLLAILKEDLPDPTADLYEFCFSDPPI 516
QY 369 DVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNRHAFNVQQLMFA 428
Db 517 TEHELVKCGLRLFLFLEINVVEKFKVPVEVLTRWMTYVRKGYRPTVYHNRHGFNVGOTWFT 576
QY 429 MUTTAGFQDILTEVEILAVIVGCLCHDHDHRTGNNAFQAKSGSALAQLYGTGATLEHIHF 488
Db 577 LLMTGRLKKYITDLEAFAMLAFAFCHDIDHRTGNNLYQMKSTSPLARLHGTG--ILERHHL 635
QY 489 NHAVMLIOSEGHNIFANLSSKEYSDLMQLLKQSILATDLYFERTEFFELYSKGE--- 545
Db 636 EYSKYLLOQESLNIFQNLKROFETVHLFEVATITADLALFKKRTMFKQIVDTCEQMQ 695
QY 546 -----YDWNINKHRDIFRSMLTACDILGAVTKPWEISQVAELVTSFEFGDRERLE 598
Db 696 SEETIKYVTSPTTKKEVIMAMMTACDLSAITKPWEVQSQVALLVANEFEQDGLERTV 755
QY 599 LKLTSPATFDRNRKDELPRQLQLEWIDISCMPLVQALVKNVVKLPMKLDVATNRKSWEL 658
Db 756 LQQQPIPMMDRSKDKDELKLVQGVDFVCTFYVKEFSRPHGEITPMLNGLQNNRVEWKS 815
QY 659 HOKRLLASTASSSSPASVMVAKED 682
Db 816 -----ABEYEAKVKVTEEE 829

RESULT 13
Q8UUY6
ID Q8UUY6 PRELIMINARY; PRT; 857 AA.
AC Q8UUY6;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Retinal PDE6 beta subunit.
GN PDE6B.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Li N., Baehr W.;
RT "Frog retina PDE6 subunits.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY044175; AAK95400.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_pplase_Hdc.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 857 AA; 99213 MW; 562B8549E5B650E8 CRC64;

Query Match 29.0%; Score 1021; DB 13; Length 857;
Best Local Similarity 33.8%; Pred. No. 2.5e-67;
Matches 228; Conservative 131; Mismatches 250; Indels 66; Gaps 11;

QY 42 HODELIQRTKTKDRFRNDEIDKTYKTKSLCMLPSSDGEIIGVAAQAINKIPEGAP 101
Db 145 HTKTKTINKDVSEDTYTSRFADELTEYKTKNLIAPIFMNGK--DVAVIVAMVK--TDGSPF 202
QY 102 TEDDEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIM 161
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1366.5	38.9		875	1	JW0106	3', 5'-cyclic-GMP p
2	1355.5	38.6		875	1	A48719	3', 5'-cyclic-GMP p
3	1080	30.1		862	2	I50186	3', 5'-cyclic-GMP p
4	1047	29.8		859	2	B34611	3', 5'-cyclic-GMP p
5	1039.5	29.6		855	2	A34810	3', 5'-cyclic-GMP p
6	1037.5	29.5		858	2	JC4520	3', 5'-cyclic-GMP p
7	1030	29.3		859	2	S13030	3', 5'-cyclic-GMP p
8	1027	29.2		856	1	A47451	3', 5'-cyclic-GMP p
9	1026	29.2		859	1	S06418	3', 5'-cyclic-GMP p
10	1025	29.2		856	2	S03762	3', 5'-cyclic-GMP p
11	1020	29.0		854	2	A43828	3', 5'-cyclic-GMP p
12	1009	28.7		853	2	A36617	3', 5'-cyclic-GMP p
13	976	27.8		800	2	S13032	3', 5'-cyclic-GMP p
14	933.5	26.6		928	1	JC2486	3', 5'-cyclic-GMP p
15	920.5	26.2		921	1	A40981	3', 5'-cyclic-nucle
16	790	22.5		393	2	T25590	3', 5'-cyclic-nucle
17	535.5	15.2		841	1	S24462	hypothetical prote
18	535.5	15.2		918	2	D88544	probable 3', 5'-cyc
19	351.5	10.8		536	2	I67945	protein R08D7.6 [i
20	365	10.4		712	2	S711626	3', 5'-cyclic-nucle
21	364	10.4		673	2	I61358	3', 5'-cyclic-nucle
22	362.5	10.3		610	2	I67946	3', 5'-cyclic-nucle
23	362.5	10.3		844	2	I53865	phosphodiesterase
24	362.5	10.3		886	2	A54442	3', 5'-cyclic-nucle
25	362	10.3		584	2	B53109	3', 5'-cyclic-nucle
26	362	10.3		672	2	I61259	3', 5'-cyclic-nucle
27	357.5	10.2		859	2	AC2089	adenylate cyclase
28	350	10.0		535	1	A46378	3', 5'-cyclic-nucle
29	350	10.0		535	1	A44161	3', 5'-cyclic-nucle

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Db 584 LVQFMKHEVLKRWILSVKKNYKKNVAYHNHRAFNATQCMFAAKGAKIQNKLTDLIEI 643
Qy 445 LAVIVGCLCHDLDRGTNNAFQKSGSALAOLYGTSTLEHHHFNHVMILQSEGHNTFA 504
Db 644 LALLIAALSHDLDRGVNNSYQSEHPALQY-CHSTMEHHHFDQCLMLNSPQNQLS 702
Qy 505 NLSKEYSDLMQLKQSLATDLTYLFERRTEFFELVSKGYDWNKKNHRDIFRSLMLTA 564
Db 703 GLSIEEYKTKLIKQAILATDLALYIKRRGEFFELIRKNQFNLDHPQKELFLAMLMTA 762
Qy 565 CDLGAVTKPWEISROVAVELVTSERPEQDGRERLEKLTPSAIFDRNRKDELPRLOLEWID 624
Db 763 CDLSAITKWPQIQRIAELVATEFFDQGRERKELNIEPTDLNREKKNKIPSMQGVGFI 822
Qy 625 SICMPLYQALVKVNVKPKMLDSVATNRSKWEEL--HOKRLLASTASSSS 672
Db 823 AICQLQYALYTHVSEDCFPDLDGCRKNQKQWALAEQOEKMLINGESQQA 872

RESULT 2
A48719
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine
N:Alternate names: PDE5A1
C:Species: Bos primigenius taurus (cattle)
C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999
C:Accession: A48719; A35807
R:McAllister-Lucas, L.M.; Sonnenburg, W.K.; Kadlecsek, A.; Seger, H.; Colbr
J. Biol. Chem. 268, 22863-22873, 1993
A:Title: The structure of a bovine lung cGMP-binding, cGMP-specific phosphodiesterase de
A:Reference number: A48719; MUID:94043054; PMID:8226796
A:Accession: A48719
A:Molecule type: mRNA
A:Residues: 1-875 <MCA>
A:Cross-references: GB:L16545
A:Experimental source: lung
A:R:Thomas, M.K.; Francis, S.H.; Corbin, J.D.
J. Biol. Chem. 265, 14971-14978, 1990
A:Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding
A:Reference number: A35807; MUID:90368672; PMID:2168396
A:Accession: A35807
A:Molecule type: protein
A:Residues: 90-101 <THO>
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosphodie
C:Keywords: alternative splicing; cGMP binding; phosphoprotein; phosphoric diester hydrol
F:602-825/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F:92/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predict

Query Match 38.6%; Score 1355.5; DB 1; Length 875;
Best Local Similarity 42.9%; Pred. No. 3.7e-84;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;

Qy 54 KDRFNDIDKLTGYKTKSLICMPTRSSDGEIIGVAQAIN-KIPEGAPFTEDEKVMQMY 112
Db 237 EDPFNAEVDQITGYKTSILICMPKINHREVVGVQAQAINKNSGGTFTKEDKDFAA 296
Qy 113 LPFCGIATSNALFAASKEYRSRALLLEVYNDLFEEQTDLEKIVKIMHRAQTLKACER 172
Db 297 LAFCGIVLHNAQLVETSLLENKRNQVLDLALIFEEOQSLEVLKIAAIIISFMQVOK 356
Qy 173 CSVLLEDIESPVVKFTKSPFELMSPKCSADAENSFK-----ESMEKSSYDML----- 220
Db 357 CTFIFIVD-----DCSDSFSSVFHMECELEKS--SDTLTRERD 393
Qy 221 ---INNSTAEVLASTGLPVNISDAYQDPFRAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 394 ANRINWYAQVKNIMEPLNIPVSKDKRFPWTNENMGNIQQCIRSLCTPIKNGKKNK 453
Qy 274 IIGVAQVNLRLDG-----KPEDDADQRLFEAFVIFCGLGINNTIWMYDQVKKSWAKQSV 328
Db 454 VIGVCQLVNMKEETTGKVKAFNRNDEQFLFEAFVIFCGLGIQNTOMYEAVERAMAKQVTL 513
Qy 329 DVLSYHATCSK---AEVDKPKAANIPLVSELAIDDIHFDDFSFLSDVADAMITAAALRMFMELG 385
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Db 514 EVLSYHSAABEETRELQSLAAAVVPSAQTLLKIDFSFSDFELSDELTALCTIRMFTDLN 573
Qy 386 MVQKFKIDYETLCRWLLTVRKNYM-VLYHNHRAFNVCOLMFAMLTITAGQDILTEVEI 444
Db 574 LVQFMKHEVLKRWILSVKKNYKKNVAYHNHRAFNATQCMFAAKGAKIQNKLTDLIEI 633
Qy 445 LAVIVGCLCHDLDRGTNNAFQKSGSALAOLYGTSTLEHHHFNHVMILQSEGHNTFA 504
Db 634 LALLIAALSHDLDRGVNNSYQSEHPALQY-CHSTMEHHHFDQCLMLNSPQNQLS 692
Qy 505 NLSKEYSDLMQLKQSLATDLTYLFERRTEFFELVSKGYDWNKKNHRDIFRSLMLTA 564
Db 693 GLSIEEYKTKLIKQAILATDLALYIKRRGEFFELIRKNQFNLDHPQKELFLAMLMTA 752
Qy 565 CDLGAVTKPWEISROVAVELVTSERPEQDGRERLEKLTPSAIFDRNRKDELPRLOLEWID 624
Db 753 CDLSAITKWPQIQRIAELVATEFFDQGRERKELNIEPTDLNREKKNKIPSMQGVGFI 812
Qy 625 SICMPLYQALVKVNVKPKMLDSVATNRSKWEEL--HOKRLLASTASSSS 672
Db 813 AICQLQYALYTHVSEDCFPDLDGCRKNQKQWALAEQOEKMLINGESSQT 862

RESULT 3
150186
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: 150186
R:Semple-Rowland, S.L.; Green, D.A.
Exp. Eye Res. 59, 365-372, 1994
A:Title: Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP
A:Reference number: 150186; MUID:95121406; PMID:7821382
A:Accession: 150186
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-862 <SEM>
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 30.1%; Score 1060; DB 2; Length 862;
Best Local Similarity 32.8%; Pred. No. 4.6e-64;
Matches 233; Conservative 139; Mismatches 251; Indels 88; Gaps 12;

Qy 25 TRLVQISGASLAERKQKHQDFLIQRTKT-----KDRFEN 59
Db 112 TRLLNVTPTS-----KFEDNLVNPDKETVPLDGIAGVVAHTKKFFENIPDVKKNNHFS 165
Qy 60 DEIDKLTGYKTKSLICMPTRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIA 119
Db 166 DYLDKTKGYTTVNNMAPI-TQGREVLAVVWALNKL-NASEFSKEDEEVFKKYNLISLV 223
Qy 120 ISNAQLFAASKEYRSRALLLEVYNDLFEEQTDLEKIVKIMHRAQTLKACERGVSLV- 178
Db 224 LRNHHTSYLVNIESRRSQMLLSANKVFEELTDIERQFHKALYTRMYLNCERYSVGLLD 283
Qy 179 -----EDIESPVVKFTKSPFELMSPKCSADAENSF-----KESME---KSSYDML 220
Db 284 MTKKEFYDEWPIRLGEAEPYKGPCTPDGREVNFYKIIDIYILHGKEETKIVTPPADHWC 343
Qy 221 INNSIAELVASTGLPVNISDAYQDPFRAEADQI--SGFHTRSVLCVPIWNHQTIGVA 278
Db 344 LISGLPYVAENGFCNMNAPADEYTFQKGPVDETGWIKNVLSLPVIVNKKKEIVGVA 403
Qy 279 QVNLRLDKGPFDDAQRLFEAFVIFCGLGINNTIWMYDQVKKSWAKQSVLDSYHATCS 338
Db 404 TFYNRKDGKPFDEYDEQIETLTQFLGNSVLNTDTYDKMKNLENKRDIAQELMYQTKAT 463
Qy 339 KAQVD--KPK-----AANIPLVSELAIDDIHFDDFSFLSDVADAMIT 375
```

Db 464 PTEVESILKYKEKLNVSIECDKDLIRILKEELPKDLELYEYFRFSPPVTEHGLIT 523
Qy 376 AALRMFMELGVMQVKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVCQLMFTAGF 435
Db 524 CGIRLFEINVEKFKPAEVLTRWYTVRGYRDITYHNHRHGFNVGQTFILMTGRI 583
Qy 436 QDILTEVEILAVIVGCLCHDLDRGTNNNAFOAKSGSALAQLYGTSALEHHHFNHVMIL 495
Db 584 KKYVTDLEAFAMVAAAFCHDIDHRGTNNLYQMKSAAPLAKLHG--SSILERHLEYSKTL 642
Qy 496 QSEGHNFANLSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGE----- 545
Db 643 QDESILNIFLNKQFETVHLFEVATIDTDLALYFKKRTMFKQIVDAIERKMETEPAIK 702
Qy 546 YDMNKNHRDIFRSMLTACDLGAVTKPWEISROVAELVTSEFFEQDRELEKLTPSA 605
Db 703 YISIDPTKKEVIMAMMTGCDLSAITKPEVQSKVALMANEFWEQDLERTVLOQOPIP 762
Qy 606 IFDRNRKDELPRLOLEWIDSCMPLYQALVKVNVKLPMLDSVATNRSKWE 656
Db 763 MMDNRKGDPLKQGVDFVCTFVYKEFSRFHKEITPMFDGLQNNRVEWK 813

RESULT 4
B34611
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jan-2000
C:Accession: B34611
R:Pittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,
Genomics 6, 272-283, 1990
A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi-
esterase
A:Reference number: A34611; MUID:90169986; PMID:2155175
A:Accession: B34611
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-859 <PI>
A:Cross-references: GB:M26061
C:Genetics:
A:Gene: GDB:PDE6A; PDEA
A:Cross-references: GDB:120265; OMIM:180071
A:Map position: 5q31.2-5q34
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 29.8%; Score 1047; DB 2; Length 859;
Best Local Similarity 33.1%; Pred. No. 3.5e-63;
Matches 229; Conservative 136; Mismatches 246; Indels 80; Gaps 12;

Qy 54 KDRFNDEIDKLTGYKTKSLCMLPIRSDGEIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 158 EDEHCFDVLITETKKNILASPMGK-DVVAIMAVNKV-DGSHFTKDEILLKYL 215
Qy 114 PFCGIATISNAQLFAASKEYERSRALLVEVNDLFEEDTLEKIYKIMHRAQTLLKCERC 173
Db 216 NFANLIMKWLHSLYLNHCETRRGQILLWSGSKVFEELTDIERQFHKALYTVRAFNLCDRY 275
Qy 174 SVLLEIDESPVVFKTSFEL-----MSPKCSADAENSF-----KESME 212
Db 276 SVGLLD-----MTKQEEFVPMVLMGEVPPYSGPRTPDGGEINFYKVIDYILHGKEDIK 330
Qy 213 ---KSSYSDWLINNSIAELVASTGLVPVNISDAYODPRDAEADQI--SGFHRSVLCVPI 267
Db 331 VIPNPPDHVALVSLPTYYAONGLICINMAPSEDFAFQKEPDLDESGWIKVLSNPI 390
Qy 268 WNSNHQITGVAQVNLNLDGKPFDDADQRLFAFVIFCGLGINNTIMYDOVKKSWAKQSV 327
Db 391 VNKKEEIVGATFYNRKDGKPFDEMDETLMESLTQFLGWSVLPDPTESMNKLENRKDIF 450
Qy 328 LDVLSYHATCSKAEDK-----FRANITPLVSELAIDDIHFD 365
Db 451 QDVIKHYVKCDNEEIQRLTKTREYVYKPEWCEBEEELAEILLOAEPLDADKYEINKHFHSD 510

Qy 366 FSLDVAAMITAAALRMFMELGVMQVKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVCQL 425
Db 511 LPLTELELVKCGIQMYVELKVDKFEHPQEAALVRFMYSLSGYRKITYHNHRHGFNVGQT 570
Qy 426 MFAMLTAGFODIITEVEILAVIVGCLCHDLDRGTNNNAFOAKSGSALAQLYGTSALEH 485
Db 571 MFSLLVTKGLKRYFTDLEALAMVTAFAFCHDIDHRGTNNLYQMKSONPLAKLHG--SSILER 629
Qy 486 HHFNHAVNIIQSEGHNFANLSKEYSDLMQLLKQSILATDLTLYFERRTEFFELVSKGE----- 542
Db 630 HHLEFGTKLDRDESILNIFLNKQFETVHLFEVATIDTDLALYFKKRTMFKQIVDOQSK 689
Qy 543 --KGEYDWN-----IKNHRDIFRSMLTACDLGAVTKPWEISROVAELVTSEFFEQDRE 595
Db 690 TYESEQEWQYMLLEQTKKEIVMAMMTACDLSAITKPEVQSKVALMANEFWEQDLE 749
Qy 596 RLEKLTPSAIFDRNRKDELPRLOLEWIDSCMPLYQALVKVNVKLPMLDSVATNRSKW 655
Db 750 RTVLQONPIPMMDNRKADLPKQGVDFVCTFVYKEFSRFHKEITPMFDGLTNNRKEW 809
Qy 656 -----EELHOKRLLASTASSSS 672
Db 810 KALADEYDAKMKVQEEKKQOOSAKSAAGN 840

RESULT 5
A34810
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain, cone - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000
C:Accession: A34810; A34809
R:Li, T.; Volpp, K.; Applebury, M.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 293-297, 1990
A:Title: Bovine cone photoreceptor cGMP phosphodiesterase structure deduced from a cd
A:Reference number: A34810; MUID:90115860; PMID:2153291
A:Accession: A34810
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-855 <LIT>
A:Cross-references: GB:M37838; NID:g163490; PIDN:AAA30687.1; PID:g163491; GB:M29465
R:Charbonneau, H.; Prusti, R.K.; Lefrong, H.; Sonnenburg, W.K.; Mullaney, P.J.; Walsh
Proc. Natl. Acad. Sci. U.S.A. 87, 288-292, 1990
A:Title: Identification of a noncatalytic cGMP-binding domain conserved in both the c
A:Reference number: A34809; MUID:90115859; PMID:2153290
A:Accession: A34809
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-855 <LIT>
A:Cross-references: GB:M37838; NID:g163490; PIDN:AAA30688.1; PID:g163493; GB:M29465
R:Charbonneau, H.; Prusti, R.K.; Lefrong, H.; Sonnenburg, W.K.; Mullaney, P.J.; Walsh
Proc. Natl. Acad. Sci. U.S.A. 87, 288-292, 1990
A:Title: Identification of a noncatalytic cGMP-binding domain conserved in both the c
A:Reference number: A34809; MUID:90115859; PMID:2153290
A:Accession: A34809
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 308-502 <CHA>
A:Cross-references: GB:M33140; NID:g163492; PIDN:AAA30688.1; PID:g163493; GB:M29465
C:Note: parts of this sequence were confirmed by protein sequencing
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 29.6%; Score 1039.5; DB 2; Length 855;
Best Local Similarity 35.5%; Pred. No. 1.1e-62;
Matches 234; Conservative 119; Mismatches 249; Indels 57; Gaps 11;

Qy 54 KDRFNDEIDKLTGYKTKSLCMLPIRSDGEIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 155 KNSHFSDFMDQGTGYVTRNLLATPIVMGK-EVLAVFMAVNVK-DASEFSKODEEVSFKYL 212
Qy 114 PFCGIATISNAQLFAASKEYERSRALLVEVNDLFEEDTLEKIYKIMHRAQTLLKCERC 173
Db 213 SFVSIILKLHNTNYLNIESRRSQLMWSANKVFEELTDVERQFHKALYTVRTYLNCRY 272
Qy 174 SVLLLD-----EDIESPVVFKTSFELMSPKCSADAENSF-----KESME---KS 214
Db 273 SIGLLDWTKEKEFYDENPVKLGEVPEYKPKTPDGRVIFIKIYDILHGKEEIKVIPTP 332
Qy 215 SYSDWLINNSIAELVASTGLVPVNISDAYODPRDAEADQI--SGFHRSVLCVPIWNSNH 272

Db 333 PMDHWLISGLTYVAENGFCNMMLNAPADEYFTFKGVPDVGWVKNVLSLPIVKNKE 392
QY 273 QIIGVAQVNLRLDGRPFDDADQRLFEAFVIFCGLGINNIMYDQVKKSWAKOSVALDVL 332
Db 393 DIVGVATYNNRKGDPFDEYDEHIAETLTQFLGWSLLNTDYKMNKLENKRDIAQEMLM 452
QY 333 YHATCSKAEDV---KFK-AANIPLVSELA-----IDDIHFDDFSLD 369
Db 453 NHTKATPDEIKSILKFEKLNIDVIEDCEEQVLTKEDLPDPRTADLYEFPFRHLPI 512
QY 370 VDMITAAALRMFMELGMVOKKIDYETLCRWLLTVRKNYRMVLYHNHRAFNVCOLMFAM 429
Db 513 EHELKGLRGLFFFEINVEKEKVPVEVLTVMYTVRKGYRAVYTHNHRHGFNVGOTMFTL 572
QY 430 LTTAGFQDILTEVEILAVIGCLCHDLHRTGNNFAQKSGSALAQLYGTSTATLEHHFN 489
Db 573 LMTGLRKKYYTDLFAFAMLAFAFCHDIDHRTGNNLYQMKSTSPARLHG-SSILERRHLE 631
QY 490 HAVMILOSEGHNIIFANLSKEYSDLMOLLKOSILATDLTYLFFERTFEFFELSVKGE---- 545
Db 632 YSKTLQDESINIFONLNKROVETVIHLFEVAIIATDLALYFKKRTMFKQIVDACEKMET 691
QY 546 -----YDWNINKNHRDIFRSMLMTACDLGAVTKPWEISROVAELVTSFEFFQGDRLLEL 599
Db 692 EEEAIKYVTIDTKKEIIMAMMTACDLSAITKPWEVSQVALLVAFWFEQGLDERTVL 751
QY 600 KLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVKLKPMLDSVATNRSKWEEL 658
Db 752 QOQPIPMMDNRKDELPLQVCFIDFVCTFVYKESRHFKEITPMLSLQNNRVKWSL 810
RESULT 6
JC4520
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain - human
C:Species: Homo sapiens (man)
C:Date: 08-Feb-1996 #sequence_revision 11-Apr-1997 #text_change 20-Jun-2000
C:Accession: S63688; JC4520
R:Reschenko, E.A.; Andreeva, S.G.; Suslova, V.A.; Smirnova, E.V.; Zagranichny, V.E.; Li
FEBS Lett. 381, 149-152, 1996
A:Title: Human cone-specific cGMP phosphodiesterase alpha' subunit: complete cDNA sequen
A:Reference number: S63688; MUID:96193933; PMID:8641425
A:Accession: S63688
A:Molecule type: mRNA
A:Residues: 1-858 <RES>
A:Cross-references: EMBL:X94354; NID:g1616594; PIDN:CAA64079.1; PID:g1149517
A:Note: Intron positions were determined by partial sequencing of genomic DNA
R:Vicizian, A.S.; Piriev, N.I.; Farber, D.B.
Gene 166, 205-211, 1995
A:Title: Isolation and characterization of a cDNA encoding the alpha' subunit of human c
A:Reference number: JC4520; MUID:96125191; PMID:8543163
A:Accession: JC4520
A:Molecule type: mRNA
A:Residues: 1-115 'V', 117-269 'S', 271-372 'P', 374-463 'L', 465-564 'O', 566-858 <VIC>
A:Cross-references: GB:U31973; NID:g940230; PIDN:AA96392.1; PID:g940231
A:Note: this sequence lacks a residue Tyr after the 231-Met, and has an additional resid
C:Genetics:
A:Gene: alpha'-pde
A:Introns: 160/3; 211/3; 241/3; 288/3; 313/3; 335/2; 357/3; 373/3; 423/3; 471/3; 494/3;
A:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
C:Keywords: cGMP binding; lipoprotein; phosphoric diester hydrolase; photoreceptor; pre
F:560-770/Domain: catalytic #status predicted <CAT>
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F:855/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 29.5%; Score 1037.5; DB 2; Length 858;
Best Local Similarity 35.1%; Pred. No. 1.5e-62;
Matches 231; Conservative 122; Mismatches 249; Indels 57; Gaps 11;

QY 54 KDRFNDEIDKLTGYKTKSLCMLPISRSDGEIIGVAQAINKIPGAPFTEDEKVMOMYL 113
Db 160 KNSHFSDFMDKQTYGTVKNLLATPIVGVK-EVLAVIMAVNKV-NASEFSKODEEVFSKYL 217
QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEQTDLEKIVKIMHRAQTLLKGCRC 173

Db 218 NFVSIILRLHHTSYMYNIESRRSOTILMNSANKVPEELTDVERQPHKALYTVRTYLCNERY 277
QY 174 SVLLL-----EDIESPVVVKTKSELMSPKCSADAENSP-----KESME---KS 214
Db 278 SIGLDMTKKEFYDENWPIKLGVEPYKGPRTDGRVNFYKIIDYILHGREIKVPIPT 337
QY 215 SYSOWLNNISIAELVASTGLPVSISDAYODPREDAEQI--SGPHRSVLCVPLWNSNH 272
Db 338 PADHWLISGLTYVAENGFCNMMLNAPADEYFTFKGVPDVGWVKNVLSLPIVKNKE 397
QY 273 QIIGVAQVNLRLDGRPFDDADQRLFEAFVIFCGLGINNIMYDQVKKSWAKOSVALDVL 332
Db 398 DIVGVATYNNRKGDPFDEYDEHIAETLTQFLGWSLLNTDYKMNKLENKRDIAQEMLM 457
QY 333 YHATCSKAEDV---KFK-AANIPLVSELA-----IDDIHFDDFSLD 369
Db 458 NHTKATPDEIKSILKFEKLNIDVIEDCEEQVLTKEDLPDPRTADLYEFPFRHLPI 517
QY 370 VDMITAAALRMFMELGMVOKKIDYETLCRWLLTVRKNYRMVLYHNHRAFNVCOLMFAM 429
Db 518 EHGLIKCGIRLFFFEINVEKEKVPVEVLTVMYTVRKGYRAVYTHNHRHGFNVGOTMFTL 577
QY 430 LTTAGFQDILTEVEILAVIGCLCHDLHRTGNNFAQKSGSALAQLYGTSTATLEHHFN 489
Db 578 LMTGLRKKYYTDLFAFAMLAFAFCHDIDHRTGNNLYQMKSTSPARLHG-SSILERRHLE 636
QY 490 HAVMILOSEGHNIIFANLSKEYSDLMOLLKOSILATDLTYLFFERTFEFFELSVKGE---- 545
Db 637 YSKTLQDESINIFONLNKROFETVIHLFEVAIIATDLALYFKKRTMFKQIVDACEQMT 696
QY 546 -----YDWNINKNHRDIFRSMLMTACDLGAVTKPWEISROVAELVTSFEFFQGDRLLEL 599
Db 697 EEEAIKYVTIDTKKEIIMAMMTACDLSAITKPWEVSQVALLVAFWFEQGLDERTVL 756
QY 600 KLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVKLKPMLDSVATNRSKWEEL 658
Db 757 QOQPIPMMDNRKDELPLQVCFIDFVCTFVYKESRHFKEITPMLSLQNNRVKWSL 815
RESULT 7
SI3030
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: SI3030
R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase al
A:Reference number: SI3030; MUID:91130581; PMID:1847109
A:Accession: SI3030
A:Molecule type: DNA
A:Residues: 1-859 <BAE>
A:Cross-references: EMBL:X60664; NID:g53587; PIDN:CAA43072.1; PID:g53588
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
Query Match 29.3%; Score 1030; DB 2; Length 859;
Best Local Similarity 32.9%; Pred. No. 5e-62;
Matches 227; Conservative 133; Mismatches 251; Indels 80; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTKSLCMLPISRSDGEIIGVAQAINKIPGAPFTEDEKVMOMYL 113
Db 158 EDEHCFDVLNLTGYQTKNLLASPMNGK-DVAIMAVNKKID-PHETRDEELIKYL 215
QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEQTDLEKIVKIMHRAQTLLKGCRC 173
Db 216 NFVNLINKVPHLSVLYHNCEFRRCOILLWSGSKVPEELTDIERQPHKALYTVRAFLNCDRY 275
QY 174 SVLLLEIDIESPVVVKTKSELMSPKCSADAENSP-----KESME---KSME 212

Db 276 SVGLLD-----MTKQKEFFDVPVLMGEAPAYSGPRTPDGRINFYKVIDYILHGKEDIK 330
 Qy 213 ---KSSYSDMLNINNSIAELVASTGLPNISDAYODPRFDAEADOT--SGFHRSVLVCPVI 267
 Db 331 VIPNPPADHWALVSGLPYVAQNLGINNAPAEDEFQKEPLDESQWMIKNVLSMPI 390
 Qy 268 WNSHQLIGVAQVNLRLDGKPPDDADORLFEAFVIFGGLGNNTIMYDQVKKSWAKOSVA 327
 Db 391 VNKKEEVGVATFYNRRDGRPFDDMDETLMSLTQFLGWSVLPNDPTYESMKNLENRKDI 450
 Qy 328 LDVLSYHATCSKAEDVKFAA-----NIPVLSLAIDDIHFD 365
 Db 451 QDIVKYHVKNDEETQILKTREVYKPEWCECEEEELAEILQRELPAEYENKHFPSD 510
 Qy 366 FSLDVSAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNYCQL 425
 Db 511 LPLTELELVKCGIQMYELRWKDFHJPQEAALYRFMSLSKGYRITYHNHRHGFNVGQT 570
 Qy 426 MFAMLTITAGFDIILTEVEILAVIVGCLHDHGRGTNNATQAKSGSLAOLYGTATLEH 485
 Db 571 MFSLLVTGKLRKRYPTDLEALAWTAAFCHDIDHRTNNLYQMKSONPLAKLHG--SSILER 629
 Qy 486 HHFNHVMILQSEGHNIFANLSKEYSDMLLKQSLATDLTLTYFERRTFFELVSKGE 545
 Db 630 HHLEFGKTLRDESLNIFQNLNRQHEHAHMDIAIATDLALYFKRTMFQKIVDQSK 689
 Qy 546 -----YDWN-----IKNHRDIERSMLMTACDLGAVTKPWEISROVAELVTSERPEQDRE 595
 Db 690 TYESTQEWTOYMMLEQTRKEIVMAMMTACDLSAITKPEWQSVQKALLVAAEFWEQDLE 749
 Qy 596 RLEKLTPSAIFDRNRKDELPRLOLEWIDTSCMPLYQALVKNVYKLPKMLDSVATNRSK 655
 Db 750 RTVLQONPIMPMDRKNKADLPKLVGFIDFVCTEYVYKEFSFHEEITPMLDGITNRRKEW 809
 Qy 656 -----EELHOKELLASTASSSS 672
 Db 810 KALADEYAKMKALEEKEKQOAAQAASGN 840

RESULT 8
 A47451
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
 C:Accession: A47451; S34290
 R:Suber, M.L.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993
 A:Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation
 A:Reference number: A47451; MUID:93248211; PMID:8387203
 A:Accession: A47451
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-856 <SUB>
 A:Cross-references: GB:223014; NID:g312327
 A:Experimental source: Irish setter, retina
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:130782, NCBIPI:130783)
 R:Clements, P.J.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S34290
 A:Accession: S34290
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-184, 'D', 186-856 <CLE>
 A:Cross-references: EMBL:223014; NID:g312327; PIDN:CA80557.1; PID:g312328
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
 C:Keywords: cGMP binding; phosphoric diester hydrolase
 F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <GNP>
 Query Match 29, 28; Score 1027; DB 1; Length 856;
 Best Local Similarity 34.38; Pred. No. 8e-62;
 Matches 232; Conservative 124; Mismatches 243; Indels 78; Gaps 12;

Qy 46 LIQQTQTKRRFNDENIDKLTGYTKSLCMLPISRSGEILIGVAAQAINKIPGAPFTEDD 105
 Db 148 MNVQMDYTECHPFSFADDELTYETRNILATPIMNGK--EVVAIVMALNKL-DGPCFTSD 205
 Qy 106 EKVQMQLPFCGIAISNAQLFAASRKEYSRALLLEVVDLFEQTDLEKIVKIMHRAQ 165
 Db 206 EDVFLKYLNFQTLNKLKYHLISYLNCEPTRRGQVLLWSANKVFEELTDIERQHFKAFTVR 265
 Qy 166 TLLKCCRSVLLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF----- 207
 Db 266 AYLCNDRYSVGLLD-----MTKEKEFFDVPVLMGEAQPYSGPRTPDGRIVFYKVIDYI 320
 Qy 208 ---KESME--KSSYSD-WLINNSIAELVASTGLPNISDAYODPRFDAEADOT--SGPHI 259
 Db 321 LHGRKEDIKVISSPADHWALASGLPTYVAESGFCINIMNTAADEMFTFEQGLDSDGWI 380
 Qy 260 RSVLCVPIWNSHQLIGVAQVNLRLDGKPPDDADORLFEAFVIFGGLGNNTIMYDQVKK 319
 Db 381 KNVLSMPTIVNKEETIVGVATFYNRRDGRPKPFDEQDEVUMESLTQFLGWSVLPNTDITYDKMKN 440
 Qy 320 SWAKOSVALDVLVSYHATCSKAEDVKFAAN-----IPLVSELA 357
 Db 441 LENRKDTAQDMVLYHVRCDEIQILPTRELKGPADCEDELGILLKEVLPGPSKFD 500
 Qy 358 IDDTDFDSDVDAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNHR 417
 Db 501 IYEFHFSDECTELELVKCGIQMYELGVKRFQIPQEVLVRFVFSVSKGYRITYHNHR 560
 Qy 418 HAFNVQMLFAMLTITAGFDIILTEVEILAVIVGCLHDHGRGTNNATQAKSGSLAOLY 477
 Db 561 HGFNVAQTMFTLLTGTGLKSYITDLEAFAMVYTAGLCHDIDHRTNNLYQMKSONPLAKLH 620
 Qy 478 GTSATLEHHNHAVMILQSEGHNIFANLSKEYSDMLLKQSLATDLTLTYFERRTTEF 537
 Db 621 G-SSILERHLEFGKFLSSEETLNIYQNLNRQHEHVIHMDIAIATDLALYFKRTMF 679
 Qy 538 FELVSKGEYDWNINHRD-----IFRSMILMTACDLGAVTKPWEISROVA 581
 Db 680 QKIVDES-----KNYEDRKSWEVLSLETTTRKEIVMAMMTACDLSAITKPEWQSVKA 733
 Qy 582 ELVTSEFPEQDRELERLEKLTPSAIFDRNRKDELPRLOLEWIDTSCMPLYQALVKNVYK 641
 Db 734 LLVAAEFWEQDLEKTLVLDQOQIPMDRKNKAAELPKLVGFIDFVCTEYVYKEFSFHEE 793
 Qy 642 KPMILDSVATNRSKWEEL 658
 Db 794 LPMEDRLQNNRKNKAL 810

RESULT 9
 S06418
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
 N:Alternate names: cGMP phosphodiesterase alpha chain
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: S06418; S27007; S00161; A34611; S08516
 R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.;
 T.M.; Bystrov, N.S.; Sevartsova, I.V.; Lipkin, V.M.
 Dokl. Biochem. 296, 303-307, 1987
 A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the
 A:Reference number: S06418
 A:Accession: S06418
 A:Molecule type: mRNA
 A:Residues: 1-859 <OVI>
 A:Cross-references: EMBL:X12756; NID:9616; PIDN:CAA31243.1; PID:9617
 A:Accession: S27007
 A:Molecule type: protein
 A:Residues: 2-11; 22-27; 32-40; 95-98; 112-115; 180-193; 248-267; 275-282; 297-306; 312-330; 36
 645-654-661-663-667-703-712-734-736; 751-760; 766-771; 787-798; 811-819 <OVC>
 A:Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nau
 R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ishchenko, K.A.; Zagranchny, V.E
 FEBS Lett. 223, 169-173, 1987
 A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the

A:Reference number: S00161; MUID:88030033; PMID:2822478

A:Accession: S00161

A:Molecule type: mRNA

A:Residues: 1-859 <OV2>

A:Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828

A:Note: part of this sequence was confirmed by protein sequencing

A:Note: 381-Val was also found

R:Pittler, S.J.; Baehr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen, Genomics 6, 272-283, 1990

A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi-

A:Reference number: A34611; MUID:90169986; PMID:2155175

A:Accession: A34611

A:Molecule type: mRNA

A:Residues: 1-193,'V',195-423,'T',425-674,'F',676-859 <PIT>

A:Cross-references: GB:M26043; NID:g162833; PIDN:AAA30443.1; PID:g162834

C:Comment: This protein is involved in the transduction and amplification of the visual

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide

C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; reti-

F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <MA

F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match 29.2%; Score 1026; DB 1; Length 859;

Best Local Similarity 32.6%; Pred. No. 9.4e-62;

Matches 225; Conservative 138; Mismatches 248; Indels 80; Gaps 12;

QY 54 KDRFENDEIKLTGYKTSLLCMPISRDGEIIGVAQAINKIPECAPTEDEDEKVMOMYL 113

DB 158 EDEHCFDFTLTETQTNILASPIINGK-DVVAIMAVNKV-DGPHTEENDEILLKYL 215

QY 114 PCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLKRCRC 173

DB 216 NFANLIMKVFHLSYLHNCETRRGQILLWSGKVFEEITDIERQFHKALYTVRAFLNCDRY 275

QY 174 SVLLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF-----KESME 212

DB 276 SVGLLD-----MTKKEFFDVPVLMGEAPYGPRTDGRINEPKYVIDILHGKEDIK 330

QY 213 ---KSSYSDWLNNISIAELVASTGLPVNISIDAYQDPREDAEQI---SGFHRSVLCVPI 267

DB 331 VIPNPPDHVALVSLPTVYVAQGLICINIMAPSEDFAFOKEPLDESGWIKNVLNPI 390

QY 268 WNSNHQIIGVAVNLNLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDOVKKSWAKOSVA 327

DB 391 VNKKEEIVGVATFYNRKDKGPFDEMDETLMESLAQFLGWSVLNPDYELMKNLENRKDIF 450

QY 328 LDVLSYHATCSKAEDV-----KFKAAINPLVSELAIDDIHFD 365

DB 451 QDMKYHVKNQNEEIQTITKTRVYGVKEPCEEEELAEILOGELPDADKYEINKFHFSD 510

QY 366 FSLVDAMITAAALRMFMELGVQKFDYETLCRWLLTVKRYNRMVLYHNHRHAFNVCOL 425

DB 511 LPLTELELVKGIQMYELKVDVDFHPIQELVAVRFMYSLSKYRITYHNHRHGFNGQT 570

QY 426 MFAMLTITAGFODITVEILAVIVCGCLCHDLDRGTNNAFQKSGSALQALYGTSATLEH 485

DB 571 MFSLVTKLRYFTDLEALAVTAAAFCHDIDHRTNNLYQMKSONPLAKLHG-SSILER 629

QY 486 HHENHAVMILQSEGNIFANLSKEYSDLMOLLQKSLATDITLYFERRTEFFELVSKG- 544

DB 630 HLEFGKTLTLDSEINLQNNRHOEHAHIMMDIAIATDIALYCKRKNFQKIVQSK 689

QY 545 ----EYDWN-----IKNHRDIFRSLMTACDLGAVTKPWEISROVAELVTSFEFOGDRE 595

DB 690 TYEQEWQNTQYMLDQTRKEIVMAAMTACDLSAITKFWQSVKALLVAEFWEQGDLE 749

QY 596 RLEKLPTSAIFDRNRKDELPRLOLEWIDTSCMPYQALVKVYNKLPMLDSVATNRKSW 655

DB 750 RTVLQONPIMDRNKADELPLKQGVDFVCTVEYKEFSRFEHEITPMLDGIITNRKEW 809

QY 656 -----ELHQKELLASTASSS 672

DB 810 KALADEYETMKGLEEKQKQAAANQAAAGS 840

RESULT 10

S30762

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000

C:Accession: S30762; S13031; S13121

R:Baehr, W.

submitted to the EMBL Data Library, June 1991

A:Reference number: S30762

A:Accession: S30762

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-856 <BAE>

A:Cross-references: EMBL:X60133; NID:g53595; PIDN:CAA42719.1; PID:g53596

R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.

FEBS Lett. 278, 107-114, 1991

A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase al

cing of the beta-subunit gene.

A:Reference number: S13030; MUID:91130581; PMID:1847109

A:Accession: S13031

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-559,'G',561-856 <BA2>

A:Cross-references: EMBL:X60133

R:Boxes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.

Nature 347, 677-680, 1990

A:Title: Retinal degeneration in the rd mouse is caused by a defect in the beta subun

A:Reference number: S13121; MUID:91015387; PMID:1977087

A:Accession: S13121

A:Molecule type: mRNA

A:Residues: 1-2,'X',4,'G',6-18,'S',20-48,'DV',51-157,'T',159-175,'C',177-231,'R',233-

A:Cross-references: EMBL:X5968; NID:g53616; PIDN:CAA39439.1; PID:g53617

C:Note: the authors translated the codon AGA for residue 232 as Glu

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotid

C:Keywords: cGMP binding; phosphoric diester hydrolase

F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 29.2%; Score 1025; DB 2; Length 856;

Best Local Similarity 34.1%; Pred. No. 1.le-61;

Matches 231; Conservative 121; Mismatches 247; Indels 78; Gaps 11;

QY 46 LIQRTKTKDRRNDKIDKLTGYKTSLLCMPISRDGEIIGVAQAINKIPEGAPFTEDD 105

DB 148 MINVDVAECFHSFSEADELTDYTKNLLSPIMNGK-DVVAVIMAVNKL-DGPCFTSED 205

QY 106 EKVQMYLPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQ 165

DB 206 EDVETKYNLNFATLNLKIYHLSYHNCETRRGQVLLWSANKVFEELTDIERQFHAKFYTVR 265

QY 166 TLLCERCSSVLLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF----- 207

DB 266 AYLNCERYSGLLD-----MTKKEFFDVPVLMGEAPYGPRTDGRINEPKYVIDYI 320

QY 208 ---KESME---KSSYSDWLNNISIAELVASTGLPVNISIDAYQDPREDAEQI---SGFHI 259

DB 321 LHGHEDIKVIPTPADHVALASGLPTVVAESGFTCNIMNASADEMFNQEGPLDSDSGWVI 380

QY 260 RSVLCVPIMNSNHQIIGVAVNLNLDGKPFDDADQRLFEAFVIFCGLGINNTIMYDOVKK 319

DB 381 KNVLSMPTVNRKEEIVGVATFYNRKDKGPFDDQDEVLMESLTQFLGWSVLNTDITYDKMK 440

QY 320 SWAKOSVALDVLSTHATCSKAEDV-----KFKAAINPLVSELA 357

DB 441 LENRKKIAQDMVLYHVRCKDEIQEILPTRDLRGLKEPADCEDELGKILKEELPGTKFD 500

QY 358 IDDIHFDDESLDAMDILTAALRMFMELGVQKFDYETLCRWLLTVKRYNRMVLYHNHR 417

DB 501 IYEFHFSDECTELELVKCGIQMYELKVDVDFHPIQELVAVRFMYSLSKYRITYHNHR 560

QY 418 HAFNVCOMFAMLTITAGFODITVEILAVIVCGCLCHDLDRGTNNAFQKSGSALQALY 477

Db 561 HGFNVAQWTFILLMTGKLSYYTDLEAFAMVTAGLCHDIDHRTNNLYQMSQNPPLAKLH 620

QY 478 GTSATLEHHHFNHVAWMIQSEGHNFANLSSKEYSDLMQLKQSLATDLTLTYFFRRTEF 537

Db 621 G-SSILERHLEFGKFLLAESLNIYQNLRRQHEHVIHLMDIAIATDLALYFKKRTMF 679

QY 538 FELVSKGEYDNKIHNRD-----IFRSMLMTACDGLGAVTWPWEISROVA 581

Db 680 QKIVDES-----KNYEDKKSWVEYLSLETTKRKEIVMAMMTACDLSAITRKPWEVQSKVA 733

QY 582 ELVTSEFFQDGRLEKLTPSAIFDRNRKDELPRLOLEWIDSTCMPLYOALYKVNKL 641

Db 734 LLVAAEFWEQDLETVLDOQPIPMMDNRKAAELPKQVGFIDFVCTFYKFEFSRFHEE 793

QY 642 KPMLDVATNRSKWBEEL 658

Db 794 LPMFDRLQNNRKWKAL 810

RESULT 11

A42828

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - human

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: A42828; S34590; S18715

R:Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R. Genomics 13, 698-704, 1992

A:Title: The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete re

A:Reference number: A42828; UID:92347868; PMID:1322354

A:Accession: A42828

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-854 <COL>

A:Cross-references: GB:S41458; NID:q252252; PIDN:AAB22690.1; PID:q252253

A:Note: sequence extracted from NCBI backbone (NCBIN:109783, NCBI:P:109784)

R:Khrantsov, N.V.; Feshchenko, E.A.; Suslova, V.A.; Shmukler, B.E.; Terpugov, B.E.; Raki

FBS Lett. 327, 275-278, 1993

A:Title: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu

A:Reference number: S34590; UID:93351644; PMID:8394243

A:Accession: S34590

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-854 <KRR>

A:Cross-references: EMBL:X66142; NID:g396492; PIDN:CAA46932.1; PID:g396493

R:Weber, B.; Riess, O.; Hutchinson, G.; Collins, C.; Lin, B.; Kowbel, D.; Andrew, S.; S

Nucleic Acids Res. 19, 6263-6268, 1991

A:Title: Genomic organization and complete sequence of the human gene encoding the beta-

A:Reference number: S18715; UID:92066478; PMID:1720239

A:Accession: S18715

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-314,'Q',316-319,'L',321-359,'R',361-697,'I',699-854 <WEB>

A:Cross-references: EMBL:X62694

C:Genetics:

A:Gene: GDB:PD56B; PDEB

A:Cross-references: GDB:125915; OMIM:180072

A:Map position: 4p16.3-4p16.3

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p

C:Keywords: cGMP binding; phosphoric diester hydrolase

F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CMP>

Query Match 29.0%; Score 1020; DB 2; Length 854;

Best Local Similarity 34.4%; Pred. No. 2.4e-61;

Matches 229; Conservative 118; Mismatches 240; Indels 78; Gaps 11;

QY 58 FNDEIDKLTGYKTSLLCMPRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQWMLPCG 117

Db 160 FSSFADELTKYTKNMLATPTMNGK-DYVAVIMAVNKL-NGFFETSEDEDFVLYKYLNEAT 217

QY 118 IATISNAQFAASRKEYSRALLEVVNDLFEEOTDEKIVKIMHRAOTLLKRCRCSVLL 177

Db 218 LYLYTHLSYLHNCETRRGQVLLWSANKVFEELTDIERQFHAKFTVTRAYLNCERSYVGL 277

QY 178 LEDIESPVVKFTKSEFLMS-----PKCSADAENSEF-----KESME---K 213

Db 278 LD-----MTKEKEFFDVMSLGMESQPSGPRTPDGRREIVFYKVIDYILHKGEEKVIPT 332

QY 214 SSYDWLNNLSIAELVASTGLPVNLSDAYQDPRDAEADQI--SGFHRSVLCVPIWNSN 271

Db 333 PSADHWAASGLPSVAESGFICTNINNASDEMFKFQEGALDDSGWLKINVLNSMPIVKK 392

QY 272 HQIIGVAQVNLRLDCKPFPDADQRIFEAFVIFCGIGINNTIMYDOVKKSWAKQSVALDVL 331

Db 393 BEIVGVATFYNRKDGKPFDEQDEVLMESITQFLGHSVMTDTYDKMKNLENKRDIAQDMV 452

QY 332 SYHATCSKAEVDKFAANIPLVSELA-----IDDTHFDDFSLD 369

Db 453 LYHVKCDRDEIQILPTRARLGKEPADCDEDELGEILKEELPGPTTFDIYEFHFSDELECT 512

QY 370 VDMITAAALRMFMELGMVQKPKIDYETLCRWLLTYRKKNYRMVLYHNHRAFNVCOLMFAM 429

Db 513 ELDLVKCGIQMYELGVVKKFOIQEVLVRFISKGYRRITYHNHRRHGFVNAQTMTFTL 572

QY 430 LTTAGFQDILTVEVILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOQLYCTSATLEHHFN 489

Db 573 LMTGKLSYYTDLEAFAMVTAGLCHDIDHRTNNLYQMSQNPPLAKLHG-SSILERHLE 631

QY 490 HAVMTLOSEGHNFANLSSKEYSDLMQLKQSLATDLTLTYFFRRTEFFELYSKGEYDWN 549

Db 632 FGKFLSEETLNIYQNLRRQHEHVIHLMDIAIATDLALYFKKRAMFOKIVDES----- 686

QY 550 IKNHRD-----IFRSMLMTACDGLGAVTWPWEISROVAELVTSSEFFQGD 593

Db 687 -KNYODKKSWEYLSLETTKRKEIVMAMMTACDLSAITKPWEVQSKVALLVAAEFQGD 745

QY 594 RERLELKUTPSAIFDRNRKDELPRLOLEWIDSTCMPLYOALYKVNKLKPMLDVATNRS 653

Db 746 LERTVLDQOPIPMMDNRKAAELPKQVGFIDFVCTFYKFEFSRFHEEILPMPDRLQNNRK 805

QY 654 KWEEL 658

Db 806 EWKAL 810

RESULT 12

A36617

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - bovine

N:Alternate names: cGMP phosphodiesterase beta chain

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 21-Jan-2000

C:Accession: A36617; S19145; S14011; S00251

R:Lipkin, V.M.; Khrantsov, N.V.; Vasilevskaya, I.A.; Atabekova, N.V.; Muradov, K.G.;

J. Biol. Chem. 265, 12955-12959, 1990

A:Title: Beta-subunit of bovine rod photoreceptor cGMP phosphodiesterase. Comparison

A:Reference number: A36617; UID:90330632; PMID:2165490

A:Accession: A36617

A:Molecule type: mRNA

A:Residues: 1-853 <LIP>

A:Cross-references: GB:J05553; NID:g162824; PIDN:AAA30440.1; PID:g162825

A:Experimental source: retina

A:Note: 40-Arg was also found

R:Lipkin, V.

submitted to the EMBL Data Library, December 1990

A:Reference number: S19145

A:Accession: S19145

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-853 <LIP>

A:Cross-references: EMBL:X57146; NID:g209; PIDN:CAA40436.1; PID:g210

R:Lipkin, V.M.; Gubanov, V.V.; Khrantsov, N.V.; Vasilevskaya, I.A.; Atabekova, N.V.;

Bloorg. Khim. 16, 118-120, 1990

A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the

A:Reference number: S14011; UID:90267525; PMID:2161230

A:Accession: S14011

A>Status: preliminary

A:Molecule type: mRNA

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat
N;Alternate names: cGMP-dependent phosphodiesterase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 05-Nov-1999
C;Accession: JC2486
R;Yang, Q.; Paskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstein, R.M.; Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994
A;Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.
A;Reference number: JC2486; MUID:95110334; PMID:7811274
A;Accession: JC2486
A;Molecule type: mRNA
A;Residues: 1-928 <YAN>
A;Cross-references: GB:U21101; NID:g706929; PIDN:AAA63683.1; PID:g706930
A;Experimental source: brain
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-nucleotide phosphodiesterase, cAMP binding; cGMP binding; homodimer; phosphoprotein;
F;643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NPD>
F;109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 26.6%; Score 933.5; DB 1; Length 928;
Best Local Similarity 33.2%; Pred. No. 2.1e-55;
Matches 211; Conservative 131; Mismatches 246; Indels 47; Gaps 12;

QY 54 KDRFND--EIDKLTGVKTKSLLCMP--RSSDGEIIGVQAQAINKIPGAPFTDEDEKVM 109
Db 297 KDTSDDDVQQLQNLGCELRAMLCVPVISRATD-QVVALACAFNKL-GGDFFTDEDERAI 354
QY 110 QMYLPCFGIAISNAQLFAASRKEYERSALLVNDLFEQTDLEKIVKIMHRAOTLLK 169
Db 355 QHCFHYTGTVLTSLAFQEKQKLCCEQALLQVAKNLFTHLDDVSVLLQELIIEARNLSN 414
QY 170 CERCSEVLLLEDIESPVVKF-----TKSFELMSPKCSADAESEKESMEKSSYSDMLINN 223
Db 415 AEICSEVFLDQNELVAKVFGVVDSEYEIRP-----ADQ 451
QY 224 SIAELVASTGLPVNISDAYODPRDAEQISGFHRSVLCVPIWNSHQLIIGVQVNLNR 283
Db 452 GIGHVATTGQILNPDAYAHPLFYRGVDDSTGFRTRNLCFPIKNSQEVIGVAELVKN 511
QY 284 LDGKPEDDADQRLFEAFVFCGGINNTIMYDQVKKSWAKQSVALLDVLSYHATCSKAED 343
Db 512 INGPWFSKFEDELATAFSIYCGISIAHSLYKKVNEAQYRSHLANEMMYHMKVSDDEYT 571
QY 344 KFRANPLVSELAIDIHFDFF-----SLDVMAMITAAALRMFMELGMOKFKIDYETLC 398
Db 572 KLLHDGTPVAAI---DSNEAFETYTPRSLPEDTSMAILQDMFMFINNYKIDCPTLA 628
QY 399 RWLLTVRKRYRMVLYHNHRAFNVCQLMFAMLTATAGFDQDILTEVEILAVIVGCLCHDLH 458
Db 629 RFCLMVRKGRDPPYHNHMAFVSHPFCYLLYKNLELSNYLEDIEIFALFISCMCHDLH 688
QY 459 RGTNNAFOAKSGSALAOLYGT-SATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQL 517
Db 689 RGTNNSFOVASKSVLAALYSSEGSVMERHFAQAIALNTGNCNIPDFHSRKDYQRMLDL 748
QY 518 LKQSILATDLTLFERTEFFELVSKGEYDWNKHNHRDIFRSMMLMTACDGLAVTKPWEIS 577
Db 749 MRDILATLAHLIRFKDLQKMAEVG-YDRNNKQHRLLCILLMTSCDLSQDTKGWKT 807
QY 578 ROVAELVTSFEFGDRLERLEKLTPSAIFDRNPKDELPRLOLEWIDSICMPLYQALVKV 637
Db 808 RKTAELVYKFFSGQDLEK-AMGNRPMEMDR-EKAYIPELOQTSFMEHIAMPIYKLLQDL 865
QY 638 NVLKLPMDSVATNRSKWEELHOKRLLASTASSSS 672
Db 866 FPKAEELYRVASNRHETKVSHTFTIRGLPSNNS 900

RESULT 15
A40981
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine
N;Alternate names: cGMP-dependent phosphodiesterase
C;Species: Bos primigenius taurus (cattle)

C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 05-Nov-1999
C;Accession: A40981; B36112; B26650; A60179; C26650
R;Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A.
J. Biol. Chem. 266, 17655-17661, 1991
A;Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase
A;Reference number: A40981; MUID:91373395; PMID:1654333
A;Accession: A40981
A;Molecule type: mRNA
A;Residues: 1-921 <SON>
A;Cross-references: GB:M73512; NID:g162829; PIDN:AAA74559.1; PID:g162830
R;Le Trong, H.; Beier, N.; Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; Biochemistry 29, 10280-10288, 1990
A;Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodiesterase
A;Reference number: A36112; MUID:91104948; PMID:2176866
A;Accession: B36112
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 592-921 <LET>
A;Accession: A36112
A;Molecule type: protein
A;Residues: 1-203; 'D', 205-477, 'Q', 479-921 <LET2>
R;Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A. Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986
A;Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterases
A;Reference number: A26650; MUID:87092242; PMID:3025833
A;Accession: B26650
A;Molecule type: protein
A;Residues: 613-632, 'L', 634-794; 808-868 <CHA>
A;Experimental source: heart
R;Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meaccl, E.; Murashima, S.; Mangan Second Messengers Phosphoproteins 13, 87-98, 1991
A;Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP
A;Reference number: A60179; MUID:92065414; PMID:1659635
A;Accession: A60179
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 311-803, 'DV', 806-921 <TAN>
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: This protein is not glycosylated.
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-nucleotide phosphodiesterase, cAMP binding; cAMP binding; cGMP binding; h F;635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NPD>
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 26.2%; Score 920.5; DB 1; Length 921;
Best Local Similarity 32.8%; Pred. No. 1.6e-54;
Matches 210; Conservative 130; Mismatches 254; Indels 47; Gaps 12;

QY 48 QROTCKDRFND--ETDKLTGVKTKSLLCMP--RSSDGEIIGVQAQAINKIPGAPFTE 103
Db 283 KKSITQLKDLTSDMOQLQSGMLGCEVQAMLCVPVISRATD-QVVALACAFNKL-GDGLFTD 340
QY 104 DDEKVMQMYLPFCGIAISNAQLFAASRKEYERSALLVNDLFEQTDLEKIVKIMHR 163
Db 341 QDEHVIQCHFYSTVLTSLAFQEKQKLCCEQALLQVAKNLFTHLDDVSVLLQELITE 400
QY 164 AQTLLKERCSEVLLLEDIESPVVKF-----TKSFELMSPKCSADAESEKESMEKSSYS 217
Db 401 ARNLNSNAEICSVELLDQNELVAKVFGVVDSEYEIRP----- 440
QY 218 DWLNNISIAELVASTGLPVNISDAYODPRDAEQISGFHRSVLCVPIWNSHQLIIGV 277
Db 441 ---ADQGIAGHVATTGQILNPDAYAHPLFYRGVDDSTGFRTRNLCFPIKNSQEVIGV 497
QY 278 AQVNLRLDGKFPDDADQRLFEAFVFCGGINNTIMYDQVKKSWAKQSVALLDVLSYHATC 337
Db 498 AELVNKINGPWFSEKFEDELATAFSIYCGISIAHSLYKKVNEAQYRSHLANEMMYHMKV 557
QY 338 SKAEVDKFAANIPVSELAIDIHFDFF-----SLDVMAMITAAALRMFMELGMOKFKI 392
Db 558 SDDEYTKLLHDGTPVAAI---DSNEAFETYTPRSLPEDTSMAILQDMFMFINNYKI 614
QY 393 DYETLCRWLLTVRKRYRMVLYHNHRAFNVCQLMFAMLTATAGFDQDILTEVEILAVIVGCL 452

Db	615	DCPTLARECLVYKGYRDPYHNNMHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCM	674
QY	453	CHDLDRGTNNAFAQKSGSALAQLYGT-SATLEHHHFNHAYMILOSEGHNIFANLSKEY	511
Db	675	CHDLDRGTNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAILNTHGCNIFDHFSCRKY	734
QY	512	SDLMOLLKQSIIATDLYFFERRTEFFELVSKGEYDWNINKNHRDIFRSMLMTACDLGAVT	571
Db	735	QRMULDMDRIIATDHLAHLRIFKDLQKMAEVG-YDRTNKQHHSLLLCLLMTSCDLSDOT	793
QY	572	KPWELSRQVAELVTSEFFEQGDRELEKLTPSAIFDRNRKDELPRLOLEWIDSTCMPLY	631
Db	794	KGWKTTRKIAELLYKEFFSQGDLEK-AMGNRPMMMDR-EKAYIPELOISEMEHIAMPIY	851
QY	632	QALVKVNVKLPMLDSVATNSKWEELHOKRLLASTASSSS	672
Db	852	KLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNS	892

Search completed: June 13, 2003, 15:49:42
Job time : 44.4875 secs

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:49 ; search time 14.0228 seconds
(without alignments)
2023.123 Million cell updates/sec

Title: US-09-663-542-1

Perfect score: 3516

Sequence: 1 MLQARPLFRNLSATQW.....ASTASSSPASVMVAKEDRN 684

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1366.5	38.9	875	1 CNSA_HUMAN	076074 homo sapien
2	1357.5	38.6	865	1 CNSA_CANFA	077746 canis famil
3	1355.5	38.6	865	1 CNSA_BOVIN	Q28156 bos taurus
4	1352	38.5	833	1 CNSA_RAT	054735 rattus norv
5	1060	30.1	862	1 CNRC_CHICK	P52731 gallus gall
6	1047.5	29.8	859	1 CNRA_HUMAN	P16499 homo sapien
7	1039.5	29.6	855	1 CNRC_BOVIN	P16586 bos taurus
8	1030	29.3	858	1 CNRA_BOVIN	P11541 bos taurus
9	1030	29.3	858	1 CNRA_MOUSE	P27664 mus musculu
10	1029.5	29.3	858	1 CNRC_HUMAN	P51160 homo sapien
11	1024	29.1	856	1 CNRB_CANFA	P33726 canis famil
12	1020	29.0	854	1 CNRB_HUMAN	P35913 homo sapien
13	1020	29.0	856	1 CNRB_MOUSE	P23440 mus musculu
14	1019	29.0	860	1 CNRA_CANFA	Q28263 canis famil
15	1009	28.7	853	1 CNRB_BOVIN	P23439 bos taurus
16	950	27.0	779	1 CN10_HUMAN	Q9Y233 homo sapien
17	934.5	26.6	941	1 CN2A_HUMAN	Q00408 homo sapien
18	933.5	26.6	928	1 CN2A_RAT	Q01062 rattus norv
19	920.5	26.2	921	1 CN2A_BOVIN	P14099 bos taurus
20	790	22.5	933	1 YBZJ_CAEEL	P91119 caenorhabdi
21	573.5	16.3	365	1 CNRA_MOUSE	Q92284 mus musculu
22	535.5	15.2	918	1 YNF6_CAEEL	P30645 caenorhabdi
23	451.5	12.8	793	1 REGA_DICDI	Q23917 dictyosteli
24	443.5	12.6	534	1 CN9A_MOUSE	Q70628 mus musculu
25	431	12.0	593	1 CN9A_HUMAN	Q76083 homo sapien
26	381	10.8	536	1 CN4C_RAT	P14644 rattus norv
27	369	10.5	712	1 CN4C_HUMAN	Q08493 homo sapien
28	364	10.4	809	1 CN4D_HUMAN	Q08499 homo sapien
29	362.5	10.3	844	1 CN4A_RAT	P54748 rattus norv
30	362.5	10.3	886	1 CN4A_HUMAN	P27815 homo sapien
31	362	10.3	672	1 CN4D_RAT	P14270 rattus norv
32	351	10.0	446	1 CN7B_MOUSE	Q9qrx1 mus musculu
33	350	10.0	535	1 CN1B_MOUSE	Q01065 mus musculu

ALIGNMENTS

RESULT 1

ID	CNSA_HUMAN	STANDARD;	PRT;	875 AA.
AC	076074; 075887; 075026; Q9Y626;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)			
DE	(CGMP-binding CGMP-specific phosphodiesterase).			
GN	PDE5A OR PDE5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A1 AND PDE5A2).			
RX	MEDLINE=98382582; PubMed=9714779;			
RA	Loughney K., Hill T.R., Florio V.A., Uher L., Rosman G.J., Wolda S.L.,			
RA	Jones B.A., Howard M.L., McAllister-Lucas L.M., Sonnenburg W.K.,			
RA	Francis S.H., Corbin J.D., Beavo J.A., Ferguson K.;			
RT	"Isolation and characterization of cDNAs encoding PDE5A, a human CGMP-			
RT	binding, CGMP-specific 3',5'-cyclic nucleotide phosphodiesterase.";			
RL	Gene 216:139-147(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A1).			
RC	TISSUE=Placenta, and Lung;			
RX	MEDLINE=98380237; PubMed=9716380;			
RA	Yanaka N., Kotera J., Ohtsuka A., Akatsuka H., Imai Y., Michibata H.,			
RA	Fujishige K., Kawai E., Takebayashi S.-I., Okumura K., Omori K.;			
RT	"Expression, structure and chromosomal localization of the human			
RT	CGMP-binding CGMP-specific phosphodiesterase PDE5A gene.";			
RL	Eur. J. Biochem. 255:391-399(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A1).			
RC	TISSUE=Prostate, and Skeletal muscle;			
RX	MEDLINE=98308101; PubMed=9642111;			
RA	Stacey P., Ruten S., Dapling A., Phillips S.C.;			
RT	"Molecular cloning and expression of human CGMP-binding CGMP-specific			
RT	phosphodiesterase.";			
RL	Biochem. Biophys. Res. Commun. 247:249-254(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM PDE5A2).			
RC	TISSUE=Lung;			
RA	Kotera J., Imai Y., Omori K.;			
RT	"Molecular cloning and characterization of human CGMP-specific			
RT	phosphodiesterase 5A2 cDNA.";			
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE			
CC	INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS			
CC	PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-			
CC	GMP.			
CC	-!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =			
CC	guanosine 5'-phosphate.			
CC	-!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR			
CC	MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT			
CC	CATALYSTS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).			

Q01066 rattus norv
P70453 mus musculu
P14646 rattus norv
Q13946 homo sapien
Q08593 rattus norv
Q9np56 homo sapien
Q07343 homo sapien
Q01061 bos taurus
Q14123 homo sapien
Q22000 caenorhabdi
Q01064 homo sapien
Q64338 mus musculu

34 350 10.0 535 1 CN1B_RAT
35 349 9.9 456 1 CN7A_MOUSE
36 349 9.9 721 1 CN4B_RAT
37 347 9.9 482 1 CN7A_HUMAN
38 346 9.8 426 1 CN7A_RAT
39 346 9.8 450 1 CN7B_HUMAN
40 345 9.8 736 1 CN4B_HUMAN
41 342.5 9.7 534 1 CN1B_BOVIN
42 340 9.7 709 1 CN1C_HUMAN
43 338.5 9.6 549 1 YST1_CAEEL
44 338 9.6 536 1 CN1B_HUMAN
45 337.5 9.6 654 1 CN1C_MOUSE

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS PDE5A1 AND PDE5A2).
RC TISSUE=Lung;
RA MEDLINE=98434620; PubMed=9756948;
RX Kotsura J., Fujishige K., Akatsuka H., Imai Y., Yanaka N., Omori K.;
RT "Novel alternative splice variants of cGMP-binding cGMP-specific
phosphodiesterase.";
RL J. Biol. Chem. 273:26982-26990(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
CC INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
CC PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
CC GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
CC MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CC CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS (BY SIMILARITY).
CC -!- ENZYME REGULATION: INHIBITED BY ZAPRINAST.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- SUBCELLULAR LOCATION: PDE5A1 AND PDE5A2 ARE LOCATED MOSTLY TO
CC SOLUBLE CELLULAR FRACTIONS AND SOME TO PARTICULATE CELLULAR
CC FRACTIONS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PDE5A1 (SHOWN HERE) AND PDE5A2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: BOTH ISOFORMS EXPRESSED ABUNDANTLY IN THE
CC CEREBELLUM, HIPPOCAMPUS, RETINA, LUNG, HEART, SPLEEN, AND THORACIC
CC ARTERY. PDE5A1, BUT NOT PDE5A2, IS ALSO ABUNDANTLY EXPRESSED IN
CC THE PYLORUS.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
CC WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
CC AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
CC ALLOSTERIC SITES (BY SIMILARITY).
CC -!- MISCELLANEOUS: CGMP-BINDING TO THE ALLOSTERIC SITES IS STIMULATED
CC BY 3-ISOBUTYL-1-METHYLXANTHINE (IBMX).
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AB008467; BAA33503.1; -;
DR EMBL; AB008468; BAA33504.1; -;
DR InterPro; IPR003018; GAF;
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; cGMP-binding; Phosphorylation; Alternative splicing;
Zinc; Repeat.
FT NP_BIND 228 311 CGMP (BY SIMILARITY).
FT NP_BIND 410 500 CGMP (BY SIMILARITY).
FT BINDING 276 276 CGMP (BY SIMILARITY).
FT BINDING 277 277 CGMP (BY SIMILARITY).
FT BINDING 289 289 CGMP (BY SIMILARITY).
FT BINDING 289 289 CGMP (BY SIMILARITY).
FT BINDING 478 478 CGMP (BY SIMILARITY).
FT DOMAIN 578 843 CATALYTIC (BY SIMILARITY).
FT MOD_RES 92 92 PHOSPHORYLATION (POTENTIAL).
FT METAL 603 603 ZINC 1 (POTENTIAL).
FT METAL 607 607 ZINC 1 (POTENTIAL).

FT	METAL	632	632	ZINC 1 (POTENTIAL).
FT	METAL	643	643	ZINC 2 (POTENTIAL).
FT	METAL	647	647	ZINC 2 (POTENTIAL).
FT	METAL	672	672	ZINC 2 (POTENTIAL).
FT	VARSPPLIC	1	40	MERGSFGAGARLRPRDQDSVEAWLDDHRRDTFFSYFVKKAT -> MLPFGHQR (IN ISOFORM PDE5A2).
SO	SEQUENCE	865 AA;	98293 MW;	F20BB37B71E93BB6 CRC64;
	Query Match	38.6%;	Score 1357.5;	DB 1; Length 865;
	Best Local Similarity	42.9%;	Pred. No. 5.3e-83;	
	Matches	278;	Conservative 129;	Mismatches 190; Indels 51; Gaps 11;
Oy	54	KDRFENDEIKLGYKTKSLICMPIRSDGIIIGVAQAIN-KIPEGAPPTDEDDKVMQMY	112	
Db	237	EDPRFAEVDQITGYTKTSILCMPIKNHRREVGVQAQIKSGNGGTFTKDEKFAAY	296	
Oy	113	LPFGGIAISNOLFAASRKEVERSRALLEVVNDLFEQTDLEKIVKVTIMHRAQTLLKCR	172	
Db	297	LAFGCIVHNAQLYETSLLENKRNQVLDLASLIFEQOQSLEVLIKKAATIIISFMQVOK	356	
Oy	173	CSVLLEIDIESPVVVKFTKSPFELSPKGSADAENEFK-----ESMEKSSYSOWL-----	220	
Db	357	CTIIVDE-----DCSDSFSVFHMECELEKLPDTLTRERDAN	395	
Oy	221	-INNSIAELVASTGLPVNISDAYQDPRF---DABAOISGPHIRSVLCVPIWN-SNHQII	275	
Db	396	RINYMAQYKVTMEPLNIPDVSKDRFPMTNENTGNVNOQICIRSLCTPIKNGKKNKI	455	
Oy	276	GVAQVLRNLDG-----KPFDDADQRLFEAFVIFCGLGINNTIMYDQVKKWAKOSVALDV	330	
Db	456	GVCOLVKNMEENTGKVPFNRENDEQFLFAFVIFCGLGIONTYEAEVAMAKOMVTLEV	515	
Oy	331	LSYHATCSKABVDKFK---AANIPLVSELAIDDDHFDQSLDQVDMITAALRMFMELGMV	387	
Db	516	LSYHASAAEETKELQSLAAAVPSAQTLLKTDTSFSDLSLETALCTIRMTDLNV	575	
Oy	388	QKFIDYETICRWLLTVRKNYRM-VLYHNWRHAFNVCOLMFAMILTAGFDILTEVEILA	446	
Db	576	QNFQMKHEVLRCWILSVKKNVKNVAVHNHRAENTACQMAALKAGKIQNKLTDLLELA	635	
Oy	447	VIVGCLCHDLHRCNTNNAFOAKSGSALAQLYGTSTALEHHFNHAVMTLOSEGHNFANL	506	
Db	636	LLIALSHDLDRGVNNSYIQRSEHPLAQLY-CHSIMEHHHFDQCLMILNPGNOILSLG	694	
Oy	507	SSKEYSDLMQLLKOSIATDLTLFYFERTEFFELVSKGEYDWNKHNKDRIFRSMLMTACD	566	
Db	695	SIEEYKTLTKIKQAILATDLALYIKRGEFFELIRKNQFNLEDPHQKELFLAMLMTACD	754	
Oy	567	LGAVTKPWEISQVAELVTSFEFGDRERLELKLTPSAIFDRNRKDELPRQLQEWIDSI	626	
Db	755	LSAITKPWPIQORIAELVATEFFDQGRERKELNTEPADLNRKKNKIPSMQVGFDAI	814	
Oy	627	CMPLYQALVKVNVKLKPMLDSVATNRSKWEEL--HOKELLASTASSSS	672	
Db	815	CLQLYEALTHVSEDCFPLLDCGRNQRKQWALAEQOEKTLINGESSQA	862	

RESULT 3
CN5A_BOVIN
ID CN5A_BOVIN STANDARD; PRT; 865 AA.
AC Q28156;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (CGB-PDE)
DE (cGMP-binding cGMP-specific phosphodiesterase).
GN PDE5A OR PDE5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=94043054; PubMed=8226796;
RA McAllister-Lucas L.M., Sonnenburg W.K., Kadlecck A., Seger D.,
RA Trong H.L., Colbran J.L., Thomas M.K., Walsh K.A., Francis S.H.,
RA Corbin J.D., Beavo J.A.;
RT "The structure of a bovine lung cGMP-binding, cGMP-specific
RT phosphodiesterase deduced from a cDNA clone.";
RL J. Biol. Chem. 268:22863-22873(1993).
RN [2]
RN METAL-BINDING.
RX MEDLINE=94357882; PubMed=8077192;
RA Francis S.H., Colbran J.L., McAllister-Lucas L.M., Corbin J.D.;
RT "Zinc interactions and conserved motifs of the cGMP-binding cGMP-
RT specific phosphodiesterase suggest that it is a zinc hydrolase.";
RL J. Biol. Chem. 269:22477-22480(1994).
RN [3]
RN MUTAGENESIS.
RX MEDLINE=96107229; PubMed=8530505;
RA McAllister-Lucas L.M., Haik T.L., Colbran J.L., Sonnenburg W.K.,
RA Seger D., Turko I.V., Beavo J.A., Francis S.H., Corbin J.D.;
RT "An essential aspartic acid at each of two allosteric cGMP-binding
RT sites of a cGMP-specific phosphodiesterase.";
RL J. Biol. Chem. 270:30671-30679(1995).
RN [4]
RN MUTAGENESIS.
RX MEDLINE=96355629; PubMed=8703039;
RA Turko I.V., Haik T.L., McAllister-Lucas L.M., Burns F., Francis S.H.,
RA Francis S.H., Corbin J.D.;
RT "Identification of key amino acids in a conserved cGMP-binding site of
RT cGMP-binding phosphodiesterases. A putative NKXnd motif for cGMP
RT binding.";
RL J. Biol. Chem. 271:22240-22244(1996).
RN [5]
RN PHOSPHORYLATION, AND MUTAGENESIS.
RX MEDLINE=98109724; PubMed=9445376;
RA Turko I.V., Francis S.H., Corbin J.D.;
RT "Binding of cGMP to both allosteric sites of cGMP-binding cGMP-
RT specific phosphodiesterase (PDE5) is required for its
RT phosphorylation.";
RL Biochem. J. 329:505-510(1998).
CC -!- FUNCTION: PLAYS A ROLE IN SIGNAL TRANSDUCTION BY REGULATING THE
CC INTRACELLULAR CONCENTRATION OF CYCLIC NUCLEOTIDES. THIS
CC PHOSPHODIESTERASE CATALYZES THE SPECIFIC HYDROLYSIS OF CGMP TO 5'-
CC GMP.
CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC -!- COFACTOR: REQUIRES DIVALENT CATIONS. ZINC IONS ARE REQUIRED FOR
CC MAXIMUM ACTIVITY. MANGANESE, MAGNESIUM AND COBALT ALSO SUPPORT
CC CATALYSIS BUT AT MUCH HIGHER CONCENTRATIONS.
CC -!- ENZYME REGULATION: MOST POTENTLY INHIBITED BY ZAPRINAST AND
CC DIPYRIDAMOLE.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN
CC WHICH CONTAINS TWO HOMOLOGOUS ALLOSTERIC CGMP-BINDING REGIONS, A
CC AND B.
CC -!- PTM: PHOSPHORYLATION IS REGULATED BY BINDING OF CGMP TO THE TWO
CC ALLOSTERIC SITES.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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CC -----
CC EMBL: L16545; AB00990.1;
CC InterPro: IPR003018; GAF.
CC InterPro: IPR003607; ME_Pplase_Hdc.

DR InterPro: IPR002073; PDEase.
DR Pfam: PF00233; PDEase; 1.
DR Pfam: PF01590; GAF; 2.
DR PRINTS: PRO0387; PDIESTERASE1.
DR SMART: SM00065; GAF; 2.
DR SMART: SM00471; Hdc; 1.
DR PROSITE: PS00126; PDEASE_I; 1.
KW Hydrolase; cGMP; cGMP-binding; Phosphorylation; zinc; Repeat.
FT MOD_RES 92 92
FT METAL 603 603
FT METAL 607 607
FT METAL 632 632
FT METAL 643 643
FT METAL 647 647
FT METAL 672 672
FT NP_BIND 228 311
FT NP_BIND 410 500
FT BINDING 276 276
FT BINDING 277 277
FT BINDING 289 289
FT BINDING 478 478
FT DOMAIN 578 843
FT MUTAGEN 276 276
FT MUTAGEN 277 277
FT MUTAGEN 277 277
FT MUTAGEN 277 277
FT MUTAGEN 289 289
FT MUTAGEN 289 289
FT MUTAGEN 290 290
FT MUTAGEN 478 478
FT FT
FT FT
SQ SEQUENCE 865 AA; 98626 MW; 2FF7144B2990B4F7 CRC64;
Query Match 38.6%; Score 1355.5; DB 1; Length 865;
Best Local Similarity 42.9%; Pred. No. 7.2e-83;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;
QY 54 KDRFNDKLTGYKTKSLCMLPIRSDEGIIIGVAQAQIN-KIPEGAPFTEDEKVMQMY 112
DB 237 EDPRFAEVDQITGYKTOSTLCMPKIHREEVGVAQAINKSGNGTFTTEKDEKFAA 296
QY 113 LPFCGIAISNAOLFASRKEYERSALLEVNDLFEEQTDLEKIVKIMHRAQTLKCE 172
DB 297 LAFGIVLHNAQLYETSLLENKRNQVLLDLASLIFEQQSLEVLKKAATITISFMQV 356
QY 173 CSVLLLEDIESPVVKFTKSPKSAENSKF-----ESMEKSSYSDWL----- 220
DB 357 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTRERD 393
QY 221 ---INNSIAELVSTGLPVNISDAYQDPRDAEADQISGFH---IRSVLCVPIWN-SNHQ 273
DB 394 ANRINYAQVVKNTMEPLNIPDVSKDRFPWTNENMGNIQQCIRSLCTPIKNGKKN 453
QY 274 IIGVAQVNLRLDG-----KPFDDADQRLPFAVIFCGLGINNTIMYDQVKKSWAKSV 328
DB 454 VIGVCQLVNMKEETTKVKAENRDEQFLFAVIFCGLGTQNTQMYEAVERAMAKQVTL 513
QY 329 DVLSYHATCSK---AEVDKFKAAIPLVSELAIDDIHFDDFSLDVSADAMITAAALRMFEL 385
DB 514 EVLSYHAAEEETRELQSLAAAVPSAQTLLKTDFSFSELSDELTAICTIRMTDLN 573
QY 386 MVQKEKIDYETLCRWLLTIVRKNYRM-VLYHNHRHAFNVQCLMFAMLTAGQDILTVEI 444
DB 574 LVQNFQMKHEVLCKWILSVKKNYKNAVYHNRHAFNTAQCMFAALKAGKIKRRLTDL 633
QY 445 LAVIVGCLCHDLDRGTNNNAFOAKSGSALAQYCTSATLEHHHNFHNAVMILOSSEHNI 504
DB 634 LALLIAALSHDLDRGVNNSTYQISEHPLAOLY-CHSIMEHHHFDQCLMILNSPGNQLS 692

RESULT 9

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=93351644; PubMed=8394243;
 RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Shmukler B.E.,
 RA Terapugov B.E., Rakitina T.V., Atabekova N.V., Lipkin V.M.;
 RT "The human rod photoreceptor cGMP phosphodiesterase beta-subunit.
 RT Structural studies of its cDNA and gene.";
 RL FEBS Lett. 327:275-278(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=93244036; PubMed=1338685;
 RA Khrantsov N.V., Feshchenko E.A., Suslova V.A., Terapugov B.E.,
 RA Rakitina T.V., Atabekova N.V., Shmukler B.E., Lipkin V.M.;
 RT "Structural studies of cDNA and the gene for the beta-subunit of cGMP
 RT phosphodiesterase from human retina.";
 RL Bioorg. Khim. 18:1551-1554(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=92347868; PubMed=1322354;
 RA Collins C., Hutchinson G., Kowbel D., Weber B., Hayden M.R.;
 RT "The human beta-subunit of rod photoreceptor cGMP phosphodiesterase:
 RT complete retinal cDNA sequence and evidence for expression in brain.";
 RL Genomics 13:698-704(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92066478; PubMed=1720239;
 RA Weber B., Riess O., Hutchinson G., Collins C., Lin B., Kowbel D.,
 RA Andrew S., Schappert K., Hayden M.R.;
 RT "Genomic organization and complete sequence of the human gene encoding
 RT the beta-subunit of the cGMP phosphodiesterase and its localisation to
 RT 4p16.3.";
 RL Nucleic Acids Res. 19:6263-6268(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 238-854 FROM N.A.
 RC TISSUE=Retinal rod cell;
 RX MEDLINE=96330350; PubMed=8768262;
 RA Suslova V.A., Suslov O.N., Kim E.E., Lipkin V.M.;
 RT "Organization of the gene for the beta-subunit of human photoreceptor
 RT cyclic GMP phosphodiesterase.";
 RL Bioorg. Khim. 22:256-263(1996).
 RN [7]
 RP VARIANT ADPR TYR-557.
 RX MEDLINE=93350628; PubMed=8394174;
 RA McLaughlin M.E., Sandberg M.A., Berson E.L., Dryja T.P.;
 RT "Recessive mutations in the gene encoding the beta-subunit of rod
 RT phosphodiesterase in patients with retinitis pigmentosa.";
 RL Nat. Genet. 4:130-134(1993).
 RN [8]
 RP VARIANT CSNB3 ASN-258.
 RX MEDLINE=94355978; PubMed=8075643;
 RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
 RT "Heterozygous missense mutation in the rod cGMP phosphodiesterase
 RT beta-subunit gene in autosomal dominant stationary night blindness.";
 RL Nat. Genet. 7:64-68(1994).
 RN [9]
 RP ERRATUM.
 RX MEDLINE=95038845; PubMed=7951329;
 RA Gal A., Orth U., Baehr W., Schwinger E., Rosenberg T.;
 RL Nat. Genet. 7:551-551(1994).
 RN [10]
 RP VARIANT ADPR ASP-576.

RX MEDLINE=96129294; PubMed=8595886;
 RA Danciger M., Blaney J., Gao Y.Q., Zhao D.Y., Heckenlively J.R.,
 RA Jacobson S.G., Farber D.B.;
 RT "Mutations in the PDE6B gene in autosomal recessive retinitis
 RT pigmentosa.";
 RL Genomics 30:1-7(1995).
 RN [11]
 RP VARIANT ADPR LYS-166; HIS-212 AND HIS-228.
 RX MEDLINE=96273603; PubMed=8698075;
 RA Gao Y.Q., Danciger M., Zhao D.Y., Blaney J., Piriev N.I., Shih J.,
 RA Jacobson S.G., Heckenlively J.H., Farber D.B.;
 RT "Screening of the PDE6B gene in patients with autosomal dominant
 RT retinitis pigmentosa.";
 RL Exp. Eye Res. 62:149-154(1996).
 RN [12]
 RP VARIANT ADPR ARG-699.
 RX MEDLINE=96140746; PubMed=8557257;
 RA Valverde D., Solans T., Grinberg D., Balcells S., Vilageliu L.,
 RA Bayes M., Chivelet P., Besmond C., Goossens M., Gonzalez-Duarte R.,
 RA Baiget M.;
 RT "A novel mutation in exon 17 of the beta-subunit of rod
 RT phosphodiesterase in two RP sisters of a consanguineous family.";
 RL Hum. Genet. 97:35-38(1996).
 RN [13]
 RP VARIANT ADPR GLN-552.
 RX MEDLINE=97114306; PubMed=8956055;
 RA Valverde D., Baiget M., Seminago R., del Rio E., Garcia-Sandoval B.,
 RA del Rio T., Bayes M., Balcells S., Martinez A., Grinberg D., Ayuso C.;
 RT "Identification of a novel R552Q mutation in exon 13 of the
 RT beta-subunit of rod phosphodiesterase gene in a Spanish family with
 RT autosomal recessive retinitis pigmentosa.";
 RL Hum. Mutat. 8:393-394(1996).
 RN [14]
 RP VARIANT ADPR ASN-535.
 RX MEDLINE=98205225; PubMed=9543643;
 RA Saga M., Mashima Y., Akeo K., Kudoh J., Oguchi Y., Shimizu N.;
 RT "A novel homozygous Ile535Asn mutation in the rod cGMP
 RT phosphodiesterase beta-subunit gene in two brothers of a Japanese
 RT family with autosomal recessive retinitis pigmentosa.";
 RL Curr. Eye Res. 17:332-335(1998).
 CC -!- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
 CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL. NECESSARY
 CC FOR THE FORMATION OF A FUNCTIONAL PHOSPHODIESTERASE HOLOENZYME.
 CC -!- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2O) =
 CC guanosine 5'-phosphate.
 CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
 CC BETA). AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF RETINITIS PIGMENTOSA
 CC OF RETINAL PHOTORECEPTOR CELLS. PATIENTS TYPICALLY HAVE NIGHT
 CC VISION BLINDNESS AND LOSS OF MIDPERIPHERAL VISUAL FIELD; AS THEIR
 CC CONDITION PROGRESSES, THEY LOOSE THEIR FAR PERIPHERAL VISUAL FIELD
 CC AND EVENTUALLY CENTRAL VISION AS WELL. RP MAY OCCUR WITH AUTOSOMAL
 CC RECESSIVE (20-25% OF CASES; ADPR) AUTOSOMAL DOMINANT (15-20% OF
 CC CASES; ADPR) OR X-LINKED (10-15% OF CASES; XRP) INHERITANCE.
 CC -!- DISEASE: DEFECTS IN PDE6B ARE A CAUSE OF CONGENITAL STATIONARY
 CC NIGHT BLINDNESS (CSNB3).
 CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
 CC -!- DATABASE: NAME-Mutations of the PDE6A/B/G genes;
 CC NOTE-Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/pdemut.htm".
 CC -----
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 CC -----
 CC EMBL; S41458; AAB22690.1; -


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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X55968; CAA39439.1; ALT_SEQ.
DR EMBL; X60133; CAA42719.1; -.
DR PIR; S13121; S13121.
DR MGD; MGI:97525; Pde6b.
DR InterPro; IPR003607; ME_Plase_HDC.
DR InterPro; IPR002073; PDease.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF00233; PDease; 1.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDease_I; 1.
KW Hydroxylase; GMP; Vision; Prenylation; Lipoprotein; Membrane;
KW Alternative splicing.
FT CHAIN 1 853
FT PROPEP 854
FT LIPID 853
FT VARSPIC 801
FT CONFLICT 5
FT CONFLICT 19
FT CONFLICT 49
FT CONFLICT 158
FT CONFLICT 176
FT CONFLICT 232
FT CONFLICT 236
FT SEQUENCE 856 AA; 98501 MW; 36777040DC7496D1 CRC64;
Query Match 29.0%; Score 1020; DB 1; Length 856;
Best Local Similarity 34.0%; Pred. No. 1.7e-60;
Matches 230; Conservative 121; Mismatches 248; Indels 78; Gaps 11;
QY 46 LIQQTQTKDRFNDIDKLTGYKTSLLCMPIRSDGEEIIGVAQAQINKIPEGAPFTEDD 105
Db 148 MINQVDVAECTHFSFADELDTYVTKNICSTPIMNGK-DVVAVINAVNKL-DGPCFTSED 205
QY 106 EKVQMOMLPFGCIATISNAQLFAASRKEYERSALLEVNDLFEETDLEKIVKTKMHRQA 165
Db 206 EDVFTKYLNFATLNLKIYHLSYLNCHTRRSQVLLWSANKVFEELTDIERQFKAFYTVR 265
QY 166 TLLKCGRCSVLLEDIESPVVKFTKSFEL-----MSPKCSADAENSF----- 207
Db 266 AYLNCERYSVGLGD-----MTKEKEFFDVPVLMGEAQPYSQPRPDGRIEIVFYKVIDYI 320
QY 208 ---KESME---KSSYSDDLNNISIAELVASTGLPNVISDAVQDPFRDAEADI---SGFHI 259
Db 321 LHGKEDIKVIPTPPADHNAALSGLTYYAESGFCINIMNASADENMFQEGPLDSDGWI 380
QY 260 RSVLCVPTWNSHQIIGVAQVNLNRDGLKPFDDADQRLFEAFVIFGLGINNTIMYDQVKK 319
Db 381 KNVLSMPVKNKEEIVGVATFYNRDKGPFDDQDQDEVLMSLTQFLGWSVLNTDTYDKMNK 440
QY 320 SWAKOSVALDVLVSYHATCSKAEVD-----KFAANIPLVSELA 357
Db 441 LENRADIADQMWLYIVRCKDQEIQLTDRLKGEPACDEDELGLKILKELPGPTKFD 500
QY 358 IDDIHFDFFSLDVAAMITAAALRMFMELGMVQKFKIDYETLGRWLTLTKRNYRMVLYHNWR 417
Db 501 IYERFVSDLECTELVVKGIQYVYELGVVRKFPQVQLVRFVSVSKAYRRITYHNWR 560
QY 418 HAFNVQCLMFAMLTAGFQDILTVEILAVIVGCLCHLDHGRGNTNNAFQAGSGSALAOLY 477

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Db 561 HGFNVNAQMTFTLLMTGKLSKYTDLEAFAMVYTAGLCHDIDHRTNNLYQMKSQNPLAKLH 620
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Db 621 G-SSTLERHLEFGFLAEESLNIYQNLNRQHEHVJHMDIAIATDLALYFKKRTWF 679
QY 538 FELVSKGEYDWNKHNHRD-----IFRSMLTACDGLGAVTKPWEISROYA 581
Db 680 QKIVDES-----KNYEDKKSWEYLSLETTTRKEIVMAMMTACDLSAITKPEVQSKVA 733
QY 582 ELVTSEFFEQDGRERLEKLTPSATFDNRKDELPRLOLELTDSTCMPLQYALVKNVKL 641
Db 734 LLVAAEFWEQGLERTVLDQQPIPMMDRNKAAELPKLVGFDFVCTFVYKFEFSRHEBI 793
QY 642 KPMLDSVATNRSKWEEL 658
Db 794 LPMFDRLONNRKRAL 810
RESULT 14
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ID CNRA_CANFA STANDARD; PRT; 860 AA.
AC Q28263; Q29470;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Rod CGMP-specific 3',5'-cyclic phosphodiesterase alpha-subunit
DE (EC 3.1.4.17) (GMP-PDE alpha).
DE PDE6A OR PDEA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96331105; PubMed=8726673;
RA Komonen B., Kylma T., Cohen R.J., Penn J.S., Paulin L., Hurwitz M.,
RA Hurwitz R.L.;
RT "Elevation of cGMP with normal expression and activity of rod
RT cGMP-PDE in photoreceptor degenerate labrador retrievers.";
RL Ophthalmic Res. 28:19-28(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98099662; PubMed=9233984;
RA Wang W., Acland G.M., Aguirre G.D., Ray K.;
RT "Cloning and characterization of the cDNA encoding the alpha-subunit
RT of cGMP-phosphodiesterase in canine retinal rod photoreceptor cells.";
RL Mol. Vision 2:3-3(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle X Briard; TISSUE=Retina;
RA Veske A., Nilsson S.E.G., Gal A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: THIS PROTEIN PARTICIPATES IN PROCESSES OF
CC TRANSMISSION AND AMPLIFICATION OF THE VISUAL SIGNAL.
CC !- CATALYTIC ACTIVITY: Guanosine 3',5'-cyclic phosphate + H(2)O =
CC guanosine 5'-phosphate.
CC !- SUBUNIT: OLIGOMER COMPOSED OF TWO CATALYTIC CHAINS (ALPHA AND
CC BETA), AN INHIBITORY CHAIN (GAMMA) AND THE DELTA CHAIN.
CC !- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 268340; CAA92763.1; -.
DR EMBL; U52868; AAB70037.1; -.

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Db 181 IESPVVKTSFELMSPKCSADAENSEPKESMEKSSYSDWLINNSIAELVASTGLPVNISD 240
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Db 241 AYQDPREDAEQIISGFHRSVLCVPIWNSNHQIIGVAQVNLNLDGKPFDDADQRLFEAF 300
Qy 301 VIFCGLGINTIMYDQVKKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLYSELAIDD 360
Db 301 VIFCGLGINTIMYDQVKKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLYSELAIDD 360
Qy 361 IHFDDFSLDAMDITAAALRMFELMGVQKFKIDYETLCRWLLTVRKKNYRMVLYHNWRHAF 420
Db 361 IHFDDFSLDAMDITAAALRMFELMGVQKFKIDYETLCRWLLTVRKKNYRMVLYHNWRHAF 420
Qy 421 NVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALAOLYCTS 480
Db 421 NVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALAOLYCTS 480
Qy 481 ATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFERTEFEFEL 540
Db 481 ATLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFERTEFEFEL 540
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Db 661 KRLLASTASSSSPASVMVAKEDRN 684
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RESULT 2

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US-09-891-216-12
; Sequence 12, Application us/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-12
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Query Match 92.4%; Score 3250; DB 10; Length 934;
Best Local Similarity 99.8%; Pred. No. 1.6e-273;
Matches 630; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 114 PFCGIAISNAQLFAASRKEYRSRALLLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 173
Db 364 PFCGIAISNAQLFAASRKEYRSRALLLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 423
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Db 424 SVLLEDIESPVVKTSFELMSPKCSADAENSEPKESMEKSSYSDWLINNSIAELVASTG 483
Qy 234 LPVNISDAYODPRDAEQIISGFHRSVLCVPIWNSNHQIIGVAQVNLNLDGKPFDDAD 293
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Qy 294 QRLFEAEVIFCGLGINTIMYDQVKKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLY 353
Db 544 QRLFEAEVIFCGLGINTIMYDQVKKSWAKOSVALDVLVSHATCSKAEDVKFKAANIPLY 603
Qy 354 SELAIDDIHFDDFSLDAMDITAAALRMFELMGVQKFKIDYETLCRWLLTVRKKNYRMVLY 413
Db 604 SELAIDDIHFDDFSLDAMDITAAALRMFELMGVQKFKIDYETLCRWLLTVRKKNYRMVLY 663
Qy 414 HNWRHAFNVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALA 473
Db 664 HNWRHAFNVCOLMFAMLTAGFQDILTEVELAVIVGCLCHDLDRGTNNAFQAKSGSALA 723
Qy 474 AQLYGTSAITLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFER 533
Db 724 AQLYGTSAITLEHHHFNHVMILQSEGHNFANLSSKEYSDLMQLLKOSILATDLTLTYFER 783
Qy 534 RTEFFELVSKGEYDWNKKNHRDIFRSMILMTACDLGAVTKPWEISROVAELVTSEFFEQG 593
Db 784 RTEFFELVSKGEYDWNKKNHRDIFRSMILMTACDLGAVTKPWEISROVAELVTSEFFEQG 843
Qy 594 RERLELKTSAIFDRNRKDELPRQLQLEWIDISICMPLYQALVKNVVKLKPMLDSVATNRS 653
Db 844 RERLELKTSAIFDRNRKDELPRQLQLEWIDISICMPLYQALVKNVVKLKPMLDSVATNRS 903
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Db 904 KWEELHOKRLLASTASSSSPASVMVAKEDRN 934
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RESULT 3

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US-09-891-216-15
; Sequence 15, Application us/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-15
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Query Match 92.4%; Score 3250; DB 10; Length 934;
Best Local Similarity 99.8%; Pred. No. 1.6e-273;
Matches 630; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 54 KDRFNDEIDKLTGYKTKSLLCMPPIRSSDGEIIGVAQAINKIPEGAPFTTDEDEKVMQMYL 113
Db 304 QDRFNDEIDKLTGYKTKSLLCMPPIRSSDGEIIGVAQAINKIPEGAPFTTDEDEKVMQMYL 363
Qy 114 PFCGIAISNAQLFAASRKEYRSRALLLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 173
Db 364 PFCGIAISNAQLFAASRKEYRSRALLLEVNDLFEETDLEKIVKIMHRAQTLLKCERC 423
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Qy 315 DOVKKSWAKQSVLDVLSYHATCSKAEDVDFKAANIPLVSELAIDDDHFDDFSLDVDAMI 374
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Qy 375 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNNRMVLYHNHRAFNVCQMLFAMLTAG 434
Db 181 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNNRMVLYHNHRAFNVCQMLFAMLTAG 240
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Db 241 FODILTEVEILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOLYGTSALEHHHFNHAMI 300
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Db 301 LQSEGHNIFANLSSKEYSDMLQKSLATDLTLTYFERR 340
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Db 301 LQSEGHNIFANLSSKEYSDMLQKSLATDLTLTYFERRTEFFELYSKGEYDWNKINHR 360
Qy 555 DIFRSLMTACDLGAVTKPWEISROVAVELTSEFFEOGDRERLEKLTPTSAIFDRNRKDE 614
Db 361 DIFRSLMTACDLGAVTKPWEISROVAVELTSEFFEOGDRERLEKLTPTSAIFDRNRKDE 420
Qy 615 LPRQLEWIDSICMPLVQALVKNVVKLPMLDSVATNRSKWEELHOKRELLASTASSSPA 674
Db 421 LPRQLEWIDSICMPLVQALVKNVVKLPMLDSVATNRSKWEELHOKRELLASTASSSPA 480
Qy 675 SVMVAKEDRN 684
Db 481 SVMVAKEDRN 490

RESULT 6

US-10-094-168B-3
; Sequence 3, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PR-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094,168B
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ. ID NOS: 7
; SOFTWARE: PERL Program
; SEQ. ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A2
US-10-094-168B-3

Query Match 50.1%; Score 1762; DB 9; Length 367;
Best Local Similarity 99.4%; Pred. No. 8.1e-145;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 195 MSPKCSADAENSKESMEKSSYSDWLNINNSTAELVASTGLPVNISTDAYQDPRFADAEADQI 254
Db 1 MSPKCSADAENSKESMEKSSYSDWLNINNSTAELVASTGLPVNISTDAYQDPRFADAEADQI 60
Qy 255 SGFHRSVLCVPINWNSHQIIGVAQVLRNLDGKPFDDADQRLPEAFVIFGGLGNNTIMY 314
Db 61 SGFHRSVLCVPINWNSHQIIGVAQVLRNLDGKPFDDADQRLPEAFVIFGGLGNNTIMY 120
Qy 315 DOVKKSWAKQSVLDVLSYHATCSKAEDVDFKAANIPLVSELAIDDDHFDDFSLDVDAMI 374
Db 121 DOVKKSWAKQSVLDVLSYHATCSKAEDVDFKAANIPLVSELAIDDDHFDDFSLDVDAMI 180

Qy 375 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNNRMVLYHNHRAFNVCQMLFAMLTAG 434
Db 181 TAALRMFMELGMWQKFKIDYETLCRWLLTVRKNNRMVLYHNHRAFNVCQMLFAMLTAG 240
Qy 435 FODILTEVEILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOLYGTSALEHHHFNHAMI 494
Db 241 FODILTEVEILAVIVGCLCHDLHRGTNNNAFOAKSGSALAOLYGTSALEHHHFNHAMI 300
Qy 495 LQSEGHNIFANLSSKEYSDMLQKSLATDLTLTYFERR 534
Db 301 LQSEGHNIFANLSSKEYSDMLQKSLATDLTLTYFERR 340

RESULT 7

US-10-115-515-23
; Sequence 23, Application US/10115515
; Publication No. US20030054992A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Corbin, Jackie D.
; Ferguson, Kenneth M.
; Francis, Sharron H.
; Radlecek, Ann
; Loughney, Kate
; McAllister-Lucas, Linda M.
; Sonnenburg, William K.
; Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,515
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/599,658
; FILING DATE: 21-Jun-2000
; APPLICATION NUMBER: 09/055,584
; FILING DATE: 4-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030054992Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-115-515-23

Query Match 38.9%; Score 1366.5; DB 9; Length 875;
Best Local Similarity 43.1%; Pred. No. 7.1e-110;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;
Qy 54 KORRFNDEIDKLTGYTKSLCPIRSSDGEIIGVAQAIN-KIPEGAPFTEDEKVNQMY 112


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Db 247 EDPFNAEVDQITGYKTOSILCMPIKHNREEVGVQAQAIN-KIPGAPFTEDDEKDFAA 306
Qy 113 LPFCGIATISNAQLFAASRKEYERSRALLEVNDLFEQTDLEKIVKKIMHRAQIILLKCE 172
Db 307 LAFGCVLHNAQLVETSLLENKRNQVLDLASLIFEEOQSLEVLKKAATATISPMQVOK 366
Qy 173 CSVLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----BSMEKSSYSDWL----- 220
Db 367 CTIFVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
Qy 221 ---INNSIAELVASTGLPVNISDAYODPRFPAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAOYVKNMTPELNPIDVSKDRFPWTTENTGNVNOQCIRSLCTPIKNGKNK 463
Qy 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVIFCGLGGINNTIMYDOVKKSWAKOSVAL 328
Db 464 VIGVCQVYNKMEENTGKVPENRNDQLEAFVIFCGLGIONTQMYEAVRAMAKQWTL 523
Qy 329 DVLVSHATCSK---AEVDKFAANIPIVSELAIDDIHDDFSLVDAMITAAALRMFMELG 385
Db 524 EVLSYHASAAEETRELQSLAAVVPVSAQTLLKIDFSFSDLEFSLDLETALETCIRMTDNL 583
Qy 386 MVQFKIDYETLCRWLLTVRKNYRM-VLYHNHRHAFNVQCLMFAMLTITAGFODILTVEI 444
Db 584 LVQNFQMKHEVLCRWILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKTONKLTDL 643
Qy 445 LAVIVGCLCHDLDRGTNNAFQKSGSALAOLYGTSTATLEHHHFNHVMILQSEGNIFA 504
Db 644 LALLIAALSHDLDRGVNSVIQSEHPLAQY-CHSIMEHHHFDQCLMLNPGNQILS 702
Qy 505 NLSKEYSDMLQKQSLATDLTYFERRTEFFELVSKGYDWNKKNRDIFRSMLMTA 564
Db 703 GLSTEEYTKTLKIQAIALATDLALYIKRRGEFFELIRKNQFNLEDPHQKELFLAMLMTA 762
Qy 565 CDLGAVTKPWISROVAELVTSERFEQDGRERLEKLTSPSAIFDRNRKDELPRLOLEWID 624
Db 763 CDLSAITKPWPQIOQRIAEVATEFFDQDGRERKELNIEPTDLMNREKKNKIPSMQVGFID 822
Qy 625 SICPMQALYKVNKPKMLDSVATNRSKWEEL--HOKRLIASTASSSS 672
Db 823 AICLQLYEALTHVSEDCFPLLDGCGRKNRQKQWQALAEQOEKMLINGESQQA 872

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RESULT 8

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US-10-094-168B-5
; Sequence 5, Application US/10094168B
; Publication No. US20030092156A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.; Harrow, Ian
; APPLICANT: Lanfear, Jerry; Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDSES
; FILE REFERENCE: PF-0623-2 CIP
; CURRENT APPLICATION NUMBER: US/10/094,168B
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/595,514
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030092156A1 g3355606
US-10-094-168B-5

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Query Match 38.9%; Score 1366.5; DB 9; Length 875;
 Best Local Similarity 43.1%; Pred. No. 7.le-110;

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Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;
Qy 54 KDRFNDIDLTKGYKTKSLLCMPIRSDGETLIGVQAQAIN-KIPGAPFTEDDEKVMOMY 112
Db 247 EDPFNAEVDQITGYKTOSILCMPIKHNREEVGVQAQAINKKSNGGTFTTEKDEKDFAA 306
Qy 113 LPFCGIATISNAQLFAASRKEYERSRALLEVNDLFEQTDLEKIVKKIMHRAQIILLKCE 172
Db 307 LAFGCVLHNAQLVETSLLENKRNQVLDLASLIFEEOQSLEVLKKAATATISPMQVOK 366
Qy 173 CSVLLEDIESPVVKFTKSFELMSPKCSADAENSFK-----BSMEKSSYSDWL----- 220
Db 367 CTIFVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
Qy 221 ---INNSIAELVASTGLPVNISDAYODPRFPAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAOYVKNMTPELNPIDVSKDRFPWTTENTGNVNOQCIRSLCTPIKNGKNK 463
Qy 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVIFCGLGGINNTIMYDOVKKSWAKOSVAL 328
Db 464 VIGVCQVYNKMEENTGKVPENRNDQLEAFVIFCGLGIONTQMYEAVRAMAKQWTL 523
Qy 329 DVLVSHATCSK---AEVDKFAANIPIVSELAIDDIHDDFSLVDAMITAAALRMFMELG 385
Db 524 EVLSYHASAAEETRELQSLAAVVPVSAQTLLKIDFSFSDLEFSLDLETALETCIRMTDNL 583
Qy 386 MVQFKIDYETLCRWLLTVRKNYRM-VLYHNHRHAFNVQCLMFAMLTITAGFODILTVEI 444
Db 584 LVQNFQMKHEVLCRWILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKTONKLTDL 643
Qy 445 LAVIVGCLCHDLDRGTNNAFQKSGSALAOLYGTSTATLEHHHFNHVMILQSEGNIFA 504
Db 644 LALLIAALSHDLDRGVNSVIQSEHPLAQY-CHSIMEHHHFDQCLMLNPGNQILS 702
Qy 505 NLSKEYSDMLQKQSLATDLTYFERRTEFFELVSKGYDWNKKNRDIFRSMLMTA 564
Db 703 GLSTEEYTKTLKIQAIALATDLALYIKRRGEFFELIRKNQFNLEDPHQKELFLAMLMTA 762
Qy 565 CDLGAVTKPWISROVAELVTSERFEQDGRERLEKLTSPSAIFDRNRKDELPRLOLEWID 624
Db 763 CDLSAITKPWPQIOQRIAEVATEFFDQDGRERKELNIEPTDLMNREKKNKIPSMQVGFID 822
Qy 625 SICPMQALYKVNKPKMLDSVATNRSKWEEL--HOKRLIASTASSSS 672
Db 823 AICLQLYEALTHVSEDCFPLLDGCGRKNRQKQWQALAEQOEKMLINGESQQA 872

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RESULT 9

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US-10-115-515-10
; Sequence 10, Application US/10115515
; Publication No. US20030054992A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Corbin, Jackie D.
; Ferguson, Kenneth M.
; Francis, Sharron H.
; Kadlec, Ann
; Loughney, Kate
; McAllister-Lucas, Linda M.
; Sonnenburg, William K.
; Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,515
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/599,658
FILING DATE: 21-Jun-2000
APPLICATION NUMBER: 09/055,584
FILING DATE: 4-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030034992Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-115-515-10

Query Match 38.6%; Score 1355.5; DB 9; Length 875;
Best Local Similarity 42.9%; Pred. No. 6.4e-109;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;
QY 54 KDRFNDKLTGKTKSLCPCIRSSDGEIIGVQAQAIN-KIPGAPPTDEDEKVMQY 112
Db 237 EDPFNAEVDQITGYKTOSILCPKHNREEVGVQAQAINKSGNGGTFTEKDEKDFAY 296
QY 113 LPFCGIAISNAOLFPAASRKEYERSALLLEVNDLFEEQTDLEKIVKIMHRAQTLLKCR 172
Db 297 LAFCGIVLHNAQLYETSLLENKRNQVLLDLASLIFEEOQSLEVLKIAATIISFQVOK 356
QY 173 CSQLLEDIESPVVTKTSFELMSPKCSADANSEK-----ESMEKSSYSDWL----- 220
Db 357 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREH 393
QY 221 ----INNSTAELVASTGLPVPNI SDAYQDPFADAEADQISGFH---IRSVLCVPIN--SNHQ 273
Db 394 ANRINYMYAQYKNTMEPLNIPDVSKDKFPTWENMGNNINQOCIRSLCTPIKNGKKN 453
QY 274 IGVQAQVNLRLDG-----KPFDDAQRLEAFVIFCGLGINTIMYDQVYKSWAKOSVAL 328
Db 454 VIGVCQVKNMEEETGKVKAFNRNDEQLEAFVIFCGLGINTQMYEAVRAMAKQMTL 513
QY 329 DYLSYHATCSK--AEVDKFAANTPLYSSELAIDDIHFDPSFLVDAMITAAALRMFMELG 385
Db 514 EYLSHASEAETEELSLAAVPSAQTILITDFSFDSOLETALCTIRMTDLN 573
QY 386 MVQKFKIDYETLCRWLLTVKKNYRM-VLYHNHRHAFNVQCMFAMLTITAGFODILTEVEI 444
Db 574 LVQVQMKHEVLCKWILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKTQKRLTDLEI 633
QY 445 LAVIVGCLCHLDHRTGNNAFOAKSGSALAQLGYTSATLEHHHFNHAYMILQSEGNIFA 504
Db 634 LALLAALSHDLDRGVNNSYTORSEHPAQLY-CHSTMEHHFPOCLMILNSPGNQILS 692
QY 505 NLSKEYSDMLQKLLATLDLTLYFERRYEFFELVSKGEYDWNKKNHRDIFRSLMTA 564
Db 693 GLSIEYKTKLIIKQAILATDLALYIKRRGEFFELIMKNROEDHPKLEFLAMLT 752
QY 565 CDLGAVTKPWEISROVAELVTSFEPQDGRERLEKLTPSAIFDRNRKDELPRLOLEWID 624
Db 753 CDLSAITRPWPIQORIAELVATEFFDQGRERKELNIEPADLMNREKKNKIPSMQVGFID 812

QY 625 SICMPLYQALVKVNVKLPMLDSVATNRSKWEEL--HOKRLASTASSSS 672
Db 813 AICLQLYEALTHVSEDCFPFLDGCRRKRNQKWOALAQOEKTLINGESSQT 862
RESULT 10
US-09-891-216-3
; Sequence 3, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: Phosphodiesterase-Like Enzyme
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Rat
US-09-891-216-3

Query Match 38.5%; Score 1352; DB 10; Length 833;
Best Local Similarity 43.8%; Pred. No. 1.2e-108;
Matches 275; Conservative 129; Mismatches 198; Indels 26; Gaps 10;
QY 54 KDRFNDKLTGKTKSLCPCIRSSDGEIIGVQAQAIN-KIPGAPPTDEDEKVMQY 112
Db 205 EDPFNAEVDQITGYKTOSILCPKHNREEVGVQAQAINKSGNGGTFTEKDEKDFAY 264
QY 113 LPFCGIAISNAOLFPAASRKEYERSALLLEVNDLFEEQTDLEKIVKIMHRAQTLLKCR 172
Db 265 LAFCGIVLHNAQLYETSLLENKRNQVLLDLASLIFEEOQSLEVLKIAATIISFQVOK 324
QY 173 CSQLLEDIESPVVTKTSFELMSPKCSADANSEKSMESKSSYSDWLINNSIAELVAST 232
Db 325 CTIFIVD--EDCPDSESRVQFQMEVEVKSSSEPLTREHANK-----INWYAYQVYKNT 376
QY 233 GLPVPNISDAYQDPF---DAEADQISGPHRSVLCVPIN--SNHQIIGVQAQVNLRLDG--- 286
Db 377 MEPLNIPDVTKDNREPWTNNNGHINTHCIRSLCTPIKNGKKNKVIQVQVQVQV 436
QY 287 ---KPFDDAQRLEAFVIFCGLGINTIMYDQVYKSWAKOSVALDVLVSYHATCSKAEVD 343
Db 437 GKIKAFNNDQGFLEAFVIFCGLGINTQMYEAVRAMAKQMTLVLEVLSYHASEAETE 496
QY 344 KFK-----AANIPLVSELAIDDIHFDPSFLVDAMITAAALRMFMELGMVQKFKIDYETLCRW 400
Db 497 ELQALAAAVPSAQTILITDFSFDSOLETALCTIRMTDLNVLQNFQMKHEVLCRW 556
QY 401 LLTVKKNYRM-VLYHNHRHAFNVQCMFAMLTITAGFODILTEVEVLAVIVGCLCHLDLHR 459
Db 557 ILSVKKNYKNVAYHNHRHAFNTAQCMFAALKAGKIQKRLTDLETLALLIALSHDLHR 616
QY 460 GTNNAFOAKSGSALAQLGYTSATLEHHHFNHAYMILQSEGNIFANLSKEYSDMLQKLL 519
Db 617 GVNNSYTORSEHPAQLY-CHSTMEHHFDOCLVNLSPGNOILSGLSIEYKTKLIIK 675
QY 520 QSLATDITLYFERKTEFFELVSKGEYDWNKKNHRDIFRSLMTACDLGAVTKPWEISRO 579
Db 676 QAILATDLALYIKRRGEFFELIRKNEFSFEDPQLEKFLAMLTACDLASITKWPPIQOR 735
QY 580 VAEIVTSSEFFQDGRERLEKLTPSAIFDRNRKDELPRLOLEWIDISCMPLYQALVKVNV 639
Db 736 IAEIVAAEFFDQGRERKELNIEPADLMNREKKNKIPSMQVGFIDAICLQLYEALTHVSE 795

Db 586 ALYSTS-TMEQHHFQSTVSIILQEGHNIFSTLSSEYEQVLEIRKAIATDLALYFQNR 644
QY 535 TEFFELVSKGEYDWNKIKNRDIFRSMMLTACDLGAVTKPWEISROVAELVTSEFEQDGR 594
Db 645 KOLEMYQTGSLNLNQSHRDRVIGLMMTACDLCSTKLPVTKLTANDIYAERWAGD- 703
QY 595 ERLEKLTPTSAIFDRNRKDELPRQLEWIDSTCMPLYQALVKVVKLPMLDSVATNRSK 654
Db 704 EMKILGIQIPMDMDRDKDEVPOGOLGFYNVAIPCYTTLTQILPPTPELLKACRDLNQ 763
QY 655 WEELHOKRLLASTASSSPASVWVAKED 682
Db 764 WEKVIRGEETATWISSPSVAOKAAASED 791

RESULT 13

US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph.
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-420-190-1

Query Match 27.0%; Score 950; DB 10; Length 779;
Best Local Similarity 33.4%; Pred. No. 9,3e-74;
Matches 210; Conservative 136; Mismatches 264; Indels 18; Gaps 7;
QY 55 DRRENDEIDKLTGYTKSLLCMPRISSDGEIIGVAQAINKIPEGAPFTEDEKVMQVLP 114
Db 170 DEREPRTGLESRTIQSVLGLPIVTAIGDLIGILELYRHWGKEA-FCLSHQEVATANLA 228
QY 115 FCGTAISNAQLFAASRKRYSRALLEVNDLFEBQTDLEKIVKIMHRAOTLLKCRCS 174
Db 229 WASVAIHVOVCRGLAKOTELNDLFDVSKTYFDNIVAIDSLLEHIMIYARNLVNADRC 288
QY 175 VLLLEDIESPVVKTSPFELMSPKCSADAENSFESMEKSSYSDWLIINNSIAELVASTGL 234
Db 289 LFQVDH-----KKNELYSDLFDIGEEKEGPRVFKTKREIFSEIEKTAGQVARTGE 339
QY 235 PWNISDAYQDPRDAEADQISGFHRSVLCVPWNINHQIIGVAQVNLRLDGKPFDDADQ 294
Db 340 VLNPIDAYADPRFNREVOLYGYTTRNLTCMPI-VSRGSGVGVQVMWNKISGSFAFKTDE 398
QY 295 RLFEAFVFCGLGNNTIMYDQVKSWAKQSVALDVLVSYHATCSKAEVDKFAANIPLVS 354
Db 399 NNFMFAVFCALAHCANMYHRIHSECIYRVTEKLSYHSICTSEEQGLMQTLPLVRL 458
QY 355 ELAIDIDHDFDLSLDVADAMITAAALRMFMELGMVOKFKIDYETLCRWLLTVRKNYRMVLYH 414
Db 459 CKETELPHFD--IGPRENMWPGIFVYVWVHRSCTSCFELEKLCRFIVMSVKKNYRRVPYH 515
QY 415 NWRAFNVCQLMFAMLTITAGQDILTEVEILAVIVGCLDHRGTNNAFQAKSGSALA 474
Db 516 NKKHATVTAHCYAILQNN--HTLTLERKGLLIACILCHDLDRHGSFNSYLQRFDHPLA 573
QY 475 OLYGTSATLEHHFNHVMILQSEGHNFANLSKEYSDLMOLLKQSTLATDLYFERR 534
Db 574 ALYSTS-TMEQHHFQSTVSIILQEGHNIFSTLSSEYEQVLEIRKAIATDLALYFQNR 632

QY 535 TEFFELVSKGEYDWNKIKNRDIFRSMMLTACDLGAVTKPWEISROVAELVTSEFEQDGR 594
Db 633 KOLEMYQTGSLNLNQSHRDRVIGLMMTACDLCSTKLPVTKLTANDIYAERWAGD- 691
QY 595 ERLEKLTPTSAIFDRNRKDELPRQLEWIDSTCMPLYQALVKVVKLPMLDSVATNRSK 654
Db 692 EMKILGIQIPMDMDRDKDEVPOGOLGFYNVAIPCYTTLTQILPPTPELLKACRDLNQ 751
QY 655 WEELHOKRLLASTASSSPASVWVAKED 682
Db 752 WEKVIRGEETATWISSPSVAOKAAASED 779

RESULT 14

US-10-094-989-4
; Sequence 4, Application US/10094989
; Patent No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-989-4

Query Match 26.6%; Score 934.5; DB 12; Length 905;
Best Local Similarity 33.1%; Pred. No. 2.6e-72;
Matches 212; Conservative 131; Mismatches 251; Indels 47; Gaps 12;
QY 48 QRQTKTKDRRND--EIDKLTGYTKSLLCMPI--RSSDGEIIGVAQAINKIPECAPFTE 103
Db 267 KKSQQLKDTSEDVQOQSGMLGCLQAMLCVPEVTSRATD-QVALACAFNKL-EGDLFTD 324
QY 104 DDEKVMQWYLFPCGTAISNAQLFAASRKRYSRALLEVNDLFEBQTDLEKIVKIMHR 163
Db 325 EDEHVIQHCFTYSTVLTSLTAFQKQKCECQALLQVAKNLFTHLDDVSVLQEIITE 384
QY 164 AOTLLKCRCSVLLLEDIESPVVVKF-----TKSELMSPKCSADAENSFESMEKSSYS 217
Db 385 ARNLSNAEICSVFLLDQNELVAKVDFGVDGVDDESEYIRIP----- 424
QY 218 DWLINNSTAELVASTGLPVNISDAYQDPRDAEADQISGFHRSVLCVPWNINHQIIGV 277
Db 425 ---ADQGIAGHVAATTGQILNIPDAYAHPLFYRGVDDSTGFRTNLCFPIKINQEVIGV 481
QY 278 AQVNLRLDGKPFDDADQRLFEAFVFCGLGNNTIMYDQVKSWAKQSVALDVLVSYHATC 337
Db 482 AELVKNKINGPWFSEFDEDLATAPSTYCGISLAHSLLYKKVNEAQYRSHLANEMMYHNV 541
QY 338 SKAEVDKFAANIPLVSELAIDDIHFDFF-----SLOVDAMITAAALRMFMELGMVOKFKI 392
Db 542 SDDEVTKLLHDIQIPVAAI---DSNFASFYTVTPRSLPEDDTSMAILSMLQDMNFNNYKI 598
QY 393 DYETLCRWLLTVRKNYRMVLYHNRHAFNVCQLMFAMLTITAGQDILTEVEILAVIVGCL 452
Db 599 DCPTLARFCLMVKRGYRDPPIYNNMHAFSVSHFCYLLYKNLELTNYLIEDIEIFALFISCM 658
QY 453 CHDLDRGTNNNAFQAKSGSALAQLYGT--SATLEHHFNHVMILQSEGHNFANLSKEY 511
Db 659 CHDLDRGTNNNSFQVASKSVLAALYSSGVSVMERHFAQATAILNTHCGNIFDHSRKY 718
QY 512 SDLMOLLKQSTLATDLYFERRTEFFELVSKGEYDWNKIKNRDIFRSMMLTACDLGAVT 571

Db 719 QRMILMDRIITLATDLAHLIRIFKDLQMAEVG-YDRNNKQHRLRLCLLMTSCDLSDDT 777
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Db 778 KGKTTTRKIAELIYKEFFSQGDLEK-AMGNRPWEMMDR-EKAYIPELOISFMEHIAMPIY 835
Qy 632 QALVKVNVKLPMLDSVATNRSKWEELHQRRLASTASSSS 672
Db 836 KLLQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNS 876

Search completed: June 13, 2003, 15:59:21
Job time : 52.0797 secs

RESULT 15
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; Sequence 2, Application US/10094989
; Patent No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: WEL, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-989-2

Query Match 26.68; Score 934.5; DB 12; Length 920;
Best Local Similarity 33.18; Pred. No. 2.7e-72;
Matches 212; Conservative 131; Mismatches 251; Indels 47; Gaps 12;
Qy 48 QROTQTKDRRND--EIDKLTGYTKTSLLCMPI--RSSDGEIIGVQAQAINKIPIEGAPFTE 103
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Qy 104 DDEKVMQMYLPFGIAISNAQLFAASRKEYERALLVNDLFEOTDLEKIVKKIMHR 163
Db 340 EDEHVIQHCFHYTSTLTSTLAFQKQKCEQALQVAKNFTLHDDVSVLLQEITE 399
Qy 164 AOTLLKCCERSVLLLEDIESPVVKF-----TKSFELMSPKCSADAENSPKESKSSYS 217
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Db 440 ---ADQGIAGHVATTGQILNPDAYAHPFLYRGVDDSTGFRNLCFPKIKNENQEVIGV 496
Qy 278 AQVNLRLDGPFDADQRLFEAFVIFCGLGINTIMTDQVKKSWAKOSVALDVLVSYHATC 337
Db 497 AELVKNKINGPWFKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHKV 556
Qy 338 SKAEVDKFAANIPLVSELATDDIHEDDF-----SLDQDAMITAAALRMFMELGMVQKFKI 392
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Qy 453 CHDLDRGTNNAFQAKSGSALAQLYGT-SATLEHHHFNHVMILQSEGHNFANLSKEY 511
Db 674 CHDLDRGTNNFSQVASKSVLAALYSSEGSVMERHFAQAIALINTHGNCIFDHFSRKDY 733
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:46:07 ; Search time 19.4761 Seconds
(without alignments)
1033.333 Million cell updates/sec

Title: US-09-663-542-1
Perfect score: 3516
Sequence: 1 MLKQARRPLRNLVSATQWK.....ASTASSSPASVMYAKEDRN 684

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2541	72.3	490	3	US-09-226-741-1
2	2541	72.3	490	4	US-09-595-514-1
3	1762	50.1	367	3	US-09-226-741-3
4	1762	50.1	367	4	US-09-595-514-3
5	1366.5	38.9	875	1	US-08-480-547A-23
6	1366.5	38.9	875	1	US-08-250-847B-23
7	1366.5	38.9	875	2	US-08-463-949A-23
8	1366.5	38.9	875	3	US-08-464-410A-23
9	1366.5	38.9	875	3	US-09-226-741-5
10	1366.5	38.9	875	4	US-09-595-514-5
11	1366.5	38.6	875	5	PCT-US94-06066-23
12	1355.5	38.6	875	1	US-08-480-547A-10
13	1355.5	38.6	875	1	US-08-250-847B-10
14	1355.5	38.6	875	2	US-08-463-949A-10
15	1355.5	38.6	875	3	US-08-464-410A-10
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19	951	27.0	803	2	US-08-951-648-4
20	951	27.0	803	4	US-09-174-437-4
21	950	27.0	779	2	US-08-951-648-6
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23	934.5	26.6	905	4	US-09-754-250-4
24	934.5	26.6	920	4	US-09-754-250-2
25	934.5	26.6	941	1	US-07-872-644-45
26	934.5	26.6	941	1	US-08-297-494-45
27	934.5	26.6	941	1	US-08-297-510-45

28	934.5	26.6	941	1	US-08-479-532-45	Sequence 45, Appl
29	934.5	26.6	941	1	US-08-455-526-45	Sequence 45, Appl
30	934.5	26.6	941	1	US-08-455-525-45	Sequence 45, Appl
31	934.5	26.6	941	3	US-09-139-491-45	Sequence 45, Appl
32	934.5	26.6	941	5	PCT-US92-03222-45	Sequence 45, Appl
33	920.5	26.2	921	1	US-07-872-644-39	Sequence 39, Appl
34	920.5	26.2	921	1	US-08-297-494-39	Sequence 39, Appl
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36	920.5	26.2	921	1	US-08-479-532-39	Sequence 39, Appl
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39	920.5	26.2	921	3	US-09-139-491-39	Sequence 39, Appl
40	920.5	26.2	921	4	US-09-754-250-5	Sequence 5, Appl
41	920.5	26.2	921	5	PCT-US92-03222-39	Sequence 39, Appl
42	920.5	26.2	942	1	US-07-872-644-43	Sequence 43, Appl
43	920.5	26.2	942	1	US-08-297-494-43	Sequence 43, Appl
44	920.5	26.2	942	1	US-08-297-510-43	Sequence 43, Appl
45	920.5	26.2	942	1	US-08-479-532-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-226-741-1
; Sequence 1, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: HSPDE10A1
US-09-226-741-1

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Qy	375	TAALRMFMELGNVQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFLMFTTAG	434	
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Qy	435	FODILTEVEILAVIVGCLCHDLDRHTNNAFOAKSGSALAQLYGTSTATLEHHHFNHVM	494	
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Qy	495	LOSEGHNIFANLSKEYSDLMQLLKQSLATLTLYFFERTEFFELVSKGEYDWNINKHR	554	
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DB 361 DIFRSLMTACDLGAVTKPWEISRQVAELVTSEFFEQDRELERLEKLTSPSAIFDRNRKDE 420
QY 615 LPRQLEWIDSCIMPLYQALYKVNKVKPKMLDSVATNRSKWEEHQKRLLASTASSSSPA 674
DB 421 LPRQLEWIDSCIMPLYQALYKVNKVKPKMLDSVATNRSKWEEHQKRLLASTASSSSPA 480
QY 675 SVMVAKEDRN 684
DB 481 SVMVAKEDRN 490
RESULT 2
US-09-595-514-1
; Sequence 1, Application US/09595514
; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDELOA1
US-09-595-514-1

Query Match 72.3%; Score 2541; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 3.2e-231; Mismatches 0; Indels 0; Gaps 0;
Matches 490; Conservative 0;
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QY 255 SGFHRSVLCVPINWNSHQIIGVAQVLNRLDGKPFDDADQRLFEAFVIFCGLGINTIMY 314
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DB 121 DOVKKSWAKQSVLDVLSYHATCSKAEDVKFAANIPLVSELAIDDIHFDDFSLDVDAMI 180
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DB 181 TAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRAFNVCQMLFAMLTAG 240
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DB 241 FQDILTEVEILAVIGCLCHDLDRGTNNAFQAKSGSALAOLYGTSALEHHHFNHAYMI 300
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QY 675 SVMVAKEDRN 684
DB 481 SVMVAKEDRN 490
RESULT 3
US-09-226-741-3
; Sequence 3, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: HSPDELOA2
US-09-226-741-3
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Best Local Similarity 99.4%; Pred. No. 6.4e-158;
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QY 435 FQDILTEVEILAVIGCLCHDLDRGTNNAFQAKSGSALAOLYGTSALEHHHFNHAYMI 494
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RESULT 4
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; Sequence 3, Application US/09595514
; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07


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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 367
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; OTHER INFORMATION: HSPDEL0A2
US-09-595-514-3

Query Match          50.1%; Score 1762; DB 4; Length 367;
Best Local Similarity 99.4%; Pred. No. 6.4e-158;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5
US-08-480-547A-23
; Sequence 23, Application US/08480547A
; Patent No. 5652131
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecsek, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,547A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565213land, Greta E.
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; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32791
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 875 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-547A-23

Query Match          38.9%; Score 1366.5; DB 1; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

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QY 113 LPECGTAINAOLFAASRKEYERSRALLEVNDLFEBQTDLEKTVKIMHRAOTLLKCR 172
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Db 367 CTIFIVDE-----DCSFSFVFHMECELEKS--SDTLTREHD 403
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Db 584 LVQNFQMKHEVLCRWLLSVKKNYRKNNVAYHNHRHAFNTAOCMEALAKAGIKQNKLTDLEI 643
QY 445 LAVIVGCLCHDLHRTGNNAFAQKSGSALAQLYGTATLEHHHFNHAFMILOSEGHNIFA 504
Db 644 LALLIAALSHDLHRTGNVNSYIQRSEHPLAQLY-CHSIMEHHHFDQCLIMILNSPGNOLS 702
QY 505 NLSKEYSDLMQLLKOSILATDITLYPERRTFELVSKGEYDNKIKNHRDIFRSLMLTA 564
Db 703 GLSIEEVKTKLTIKOAILATDLALYIKRGEFFELIRKQNFULEDPHQELFLAMLMTA 762
QY 565 CDLGAVTKPWEISQVAELVTSFEQGRERERLEKLTPSAIFDRNKKDELPRQLQLEWID 624
Db 763 CDLSAITKPWPIQOIAELVATEFFDQGRERERLEKLTPSAIFDRNKKDELPRQLQLEWID 822
QY 625 SICMPLYQALVKVNVKLPMLDSVATNRSKWEEL--HQRLLASTASSSS 672
Db 823 AICQLYEALTHVSEDCFPULLDGCGRNKRQKQALAEQQEKMLINGESGQA 872

RESULT 6
US-08-250-847B-23
; Sequence 23, Application US/08250847B
; Patent No. 5702936
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecsek, Ann
```



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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464.410A
: FILING DATE: June 5, 1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 6037119and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/32705
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 875 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-464-410A-23

Query Match      38.9%; Score 1366.5; DB 3; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12

QY 54 KDRFNEIDIKLTGVTKSLICMPIRSSDGETIIGVAQATN-KIPEGAPETEDDEKVMQY 172
Db 247 EDPFRNAEVDGITGKTSIOILCIPKIHREEVGVQAQANKKSGNGGTETEKDEKFAAY 306
QY 113 LPFCGIATISNAQLFAASRKEYERSRALLFVNDLFEEQTDLEKIVKIMHRAQTLLKCBR 172
Db 307 LAFCGVLHNAQLYETSLLENKRNQVLLDLASLIFEEOQSLEVLKIAATIISFPMQVK 366
QY 173 CSVLLEDIESPVVKFTKSFELMSPKCSADAENSPK-----ESMEKSSYSDWL----- 220
Db 367 CTIFIVDR-----DCSDSFSSVFHMECEELEKS--SDTLTREHD 403
QY 221 --TNNSTAEVLVASTGLPVNTSDAYQDPFDEADAEQISGFH--IRSVLCVPIWN--SNHQ 273
Db 404 ANKINMYAQVYKNTMPELNPIDVSKDKRFPWTNTGVNVQOCIRSLCTPIKNGKKK 463
QY 274 IIGVAQLNRLDG-----KPFDDADQRIFEAFVIFCGLGINNTIMYDQVKKSWAKOSVAL 328
Db 464 VIGVCQLNKMKEENTGKVKPENRNDQGLEAFVIFCGLGIGTQNTQMYEAVERAMAKQMTL 523
QY 329 DVLSYHATCSK---AEVDKFKRANPTPLVSELAIDDIHDPDFSLDVDAMITAAALRMFMELG 395
Db 524 EVLSYHASAAEETRELOSAAAQVPSAQTLLKIDFSFDSFELSDELTAICTIRMTFDLN 583
QY 386 MVQRFKIDYETLCRWLLTVRKNYRM-VLYHNHNRHAFNVQCLFMAMLTTAGFODILTEVEI 444
Db 584 LVQNFQMKHEVLCRWILSVKKNYKRNVAYNHNRHAFNTAQCFWAAKACKIQNKLTDLLEI 643
QY 445 LAVTVGCLCHDLDRGTNNATFOAKSGSALAQLYGTSATLLEHHHFNHNAVMILOSEGHNIFA 504
Db 644 LALLIALSHDLDRHGVSNNYSIQRSEHPLAQLY-CHSIMEHHHFDQCLMLSPNGQILS 702
QY 505 NLSKEYSDMLQKLLQSTLATDLTLYFRRTRTEFFELVSKGYDWNKINHRDIFRSLMNTA 564
Db 703 GLSIEEYKTKUKIQAIALTDALYIKRGEFFELIRKQNFLEDPHQKELFLAMLMTA 762
QY 565 CDLGAVTKPWEISROVAELVTSFEFQEGDRERLEKLTPSAIFDRNRKDELPRLQLEWID 624
Db 763 CDLSAITKPPWLPQORIAELVATEPFDQGRERKELNIETDLMNREKKNKIPSMQVGFID 822
QY 625 SICMPLVQALVKVNVKLLKPMLDVSATNRSKWEEL--HQRKLLASTASSSS 672
Db 823 AICQLVEALTHVSDCEPLFLDGCRRKQKQWALAEQQEKMLINGESGOA872

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RESULT 9
US-09-22

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; Sequence 5, Application US/09226741
; Patent No. 6100037
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623 US
; CURRENT APPLICATION NUMBER: US/09/226,741
; CURRENT FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 875
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: GI 3355606
; US-09-226-741-5

Query Match      38.9%; Score 1366.5; DB 3; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

QY      54 KDRFNDKLTGYKTKSLCMLPIRSSDGEIIGVAQAIN-KIPEGAPETEDDEKVMQY 112
Db      247 EDPRFNAEQDITGYKTSILCMLPIKHNREVVGVVAQAINKKSGNGTTERDEKDFAY 306
QY      113 LPFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCR 172
Db      307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOQSLEVLKKAATIISEFQVOK 366
QY      173 CSVLLLEDIESPVVKTFKSFELMSPKCSADAENSK-----ESMEKSSYSDWL----- 220
Db      367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
QY      221 ---INNSIAELVASTGLPVPNISDAYQDPFDEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db      404 ANKINMYAQYKNTMEPLNIPDVSKDKRPWTENTGNVNOQCIRSLCTPIKNGKKNK 463
QY      274 IIGVAQVLRNLDG-----KPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKOSVAL 328
Db      464 VIGVQCLVNKMEENTGKVPFRNRNDQFLEAFVFCGLGIQNTQMYEAVERAMAKQMTL 523
QY      329 DVLSTHATCSK---AEVDKFAANIPLVSELAIDDDIHDFDSDLDVDAMITAAALRMFELG 385
Db      524 EVLSYHASAAEETRELQSLAAAVPSAOTLKITDFSDFELSDELTAICTIRMTDLN 583
QY      386 MVOKFKIDYETLCRWLLTVRKNYRM-VLYHNRHAFNVQCLMFAMLTAGFODILTEVEI 444
Db      584 LVQNFQMKHEVLCRWILSVKKNYKKNVAYHNRHAFNTAQCFMFAALKAGKIQNKLTDLFI 643
QY      445 LAVIVGCLCHDLHGRGTNNAFQAKSGSALAQLYGTSTATLEHHHFNHVMILQSEGNIFA 504
Db      644 LALLIAALSHDLHGRGVNNSYIQRSEHPLAQLY-CHSIMEHHHFDQCLMLNSPGNQILS 702
QY      505 NLSKEYSDMLQKLSILATDILTYFERRTFFELVSKGEYDWNINKNRDIFRSLMFTA 564
Db      703 GLSIEYKTKLIIKQAILATDILTYIKRGEFFELIRKQNFLENPHOKELFLAMLFTA 762
QY      565 CDLGAVTKPWEISROVAELVTSEFFEQGRERLEKLTSPSAIFDRNRKDELPRLOLEWID 624
Db      763 CDLSAITKPWPQIQRIAELVATEFFEQGRERKELNIEPTDLNREKKNKIPSMQVGFID 822
QY      625 STCMPLQYALVKNVKKLPMDSVATNRSKWEL--HQKRLLASTASSS 672
Db      823 AICQLQYEAETHVSEDCFPFLDGCRRNRQKQWALAEQOEKMLINGESGQA 872
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RESULT 10

US-09-595-514-5

; Sequence 5, Application US/09595514

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; Patent No. 6416991
; GENERAL INFORMATION:
; APPLICANT: Phillips, Stephen C.
; APPLICANT: Lanfear, Jerry
; APPLICANT: Fawcett, Lindsay
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: HUMAN CYCLIC NUCLEOTIDE PDES
; FILE REFERENCE: PF-0623-1 CIP
; CURRENT APPLICATION NUMBER: US/09/595,514
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/226,741
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 875
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: GI 3355606
; US-09-595-514-5

Query Match      38.9%; Score 1366.5; DB 4; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

QY      54 KDRFNDKLTGYKTKSLCMLPIRSSDGEIIGVAQAIN-KIPEGAPETEDDEKVMQY 112
Db      247 EDPRFNAEQDITGYKTSILCMLPIKHNREVVGVVAQAINKKSGNGTTERDEKDFAY 306
QY      113 LPFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCR 172
Db      307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOQSLEVLKKAATIISEFQVOK 366
QY      173 CSVLLLEDIESPVVKTFKSFELMSPKCSADAENSK-----ESMEKSSYSDWL----- 220
Db      367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403
QY      221 ---INNSIAELVASTGLPVPNISDAYQDPFDEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db      404 ANKINMYAQYKNTMEPLNIPDVSKDKRPWTENTGNVNOQCIRSLCTPIKNGKKNK 463
QY      274 IIGVAQVLRNLDG-----KPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKOSVAL 328
Db      464 VIGVQCLVNKMEENTGKVPFRNRNDQFLEAFVFCGLGIQNTQMYEAVERAMAKQMTL 523
QY      329 DVLSTHATCSK---AEVDKFAANIPLVSELAIDDDIHDFDSDLDVDAMITAAALRMFELG 385
Db      524 EVLSYHASAAEETRELQSLAAAVPSAOTLKITDFSDFELSDELTAICTIRMTDLN 583
QY      386 MVOKFKIDYETLCRWLLTVRKNYRM-VLYHNRHAFNVQCLMFAMLTAGFODILTEVEI 444
Db      584 LVQNFQMKHEVLCRWILSVKKNYKKNVAYHNRHAFNTAQCFMFAALKAGKIQNKLTDLFI 643
QY      445 LAVIVGCLCHDLHGRGTNNAFQAKSGSALAQLYGTSTATLEHHHFNHVMILQSEGNIFA 504
Db      644 LALLIAALSHDLHGRGVNNSYIQRSEHPLAQLY-CHSIMEHHHFDQCLMLNSPGNQILS 702
QY      505 NLSKEYSDMLQKLSILATDILTYFERRTFFELVSKGEYDWNINKNRDIFRSLMFTA 564
Db      703 GLSIEYKTKLIIKQAILATDILTYIKRGEFFELIRKQNFLENPHOKELFLAMLFTA 762
QY      565 CDLGAVTKPWEISROVAELVTSEFFEQGRERLEKLTSPSAIFDRNRKDELPRLOLEWID 624
Db      763 CDLSAITKPWPQIQRIAELVATEFFEQGRERKELNIEPTDLNREKKNKIPSMQVGFID 822
QY      625 STCMPLQYALVKNVKKLPMDSVATNRSKWEL--HQKRLLASTASSS 672
Db      823 AICQLQYEAETHVSEDCFPFLDGCRRNRQKQWALAEQOEKMLINGESGQA 872
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RESULT 11

PCT-US94-06066-23

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Sequence 23, Application PC/TUS9406066
GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Washington
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06066
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32083
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-06066-23

Query Match 38.9%; Score 1366.5; DB 5; Length 875;
Best Local Similarity 43.1%; Pred. No. 5.5e-120;
Matches 280; Conservative 129; Mismatches 186; Indels 55; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTSLLCMPIRSSDGLIIGVQAQAIN-KIPGAPFTDEDEKVMQMY 112
Db 247 EDPRNAEVDQITGYKTOSILCMPIKNHREEVGVQAQAINKSGNGGTFTEKDKFAAY 306

QY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVYNDLFEEQTDLEKIVKIMHRAQTLLKCR 172
Db 307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOOSLEVLKKAATIIISPMQVOK 366

QY 173 CSVLLIEDIESPVVKTFSFELMSPKCSADAENSPK-----ESMEKSSYSDDL----- 220
Db 367 CTIFIVDE-----DCSDSFSSVFHMECELEKS--SDTLTREHD 403

QY 221 ---INNSTAELVASTGLPNISDAVDPRFADAEADQISGFH---IRSVLCVPIWN-SNHQ 273
Db 404 ANKINMYAQVKNMTPELNPIDVSKDRFPWTTENTGNVQOQIRSLCTPIKNGKNK 463

QY 274 IIGVQVNLRLDG-----KPFDDADQRLFEAFVFCGLGINNTIMYDQVKKSWAKOSVAL 328
Db 464 VIGVQVNLKMEENTGKVKPNRNDEQFLFAVIFCGLCIQNTQYEAVERAMAKQWTL 523

QY 329 DVLSVHATCSK---AEVDKFAANIPVLSLAIDDIHEDFSLDSDVAMITAAALRMFMELG 385
Db 524 EVLSVHASAAEETRELQSLAAAVVPSAQTUKITDFSDFLSDLEALCTIRMTDLN 583

QY 386 MVQEKIDYETLCRWLLTVKRNRM-VLYHNHRHAFNVQCLMFAMLTITAGFQDILTEVEI 444
Db 584 LVQNFQMKHEVLRCWILSVKKNRYNVAIHNHRHAFNTAQCMAFALKAGKIQNKLTDL 643

QY 445 LAVIVGCLCHDLDRGTNNNAFOAKSGSALAQLYGTSTATLEHHHFNHAYMILQSEGHNIFA 504
Db 644 LALLTAALSHDLDRGVNNSYIQRSEHPLAQLY-CHSIMEHHHFDQCLMILNSPGNQILS 702

QY 505 NLSKEYSDLMOLLKOSTLATDLTYTFERRTEFFELVSKGEYDMNKKHNRDIFRSLMWT 564
Db 703 GLSIEEYKTKLIIKQAILATDLALYIKRRGFEFFELIRKNQFNEDPHQKELFLAMLMT 762

QY 565 CDLGAVTKPWEISROVAELVTSEFFEQDGRERLEKLTPTSAIFDRNRKDELPRLOLEWID 624
Db 763 CDLSAITRPWPIQQRIAEVLATEFFDQGRERKELNIEPTDLMNREKKNKIPSMQVGFID 822

QY 625 STCMPLYQALVKNVVKLPMLDSVATNRSKWEEEL--HOKRLLASTASSSS 672
Db 823 AICLQLYEALTVHSEDCEPFLDGCGRKQKQWQALAEQOEKMLINGESGQA 872

RESULT 12
US-08-480-547A-10
Sequence 10, Application US/08480547A
Patent No. 5652131
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Corbin, Jackie D.
APPLICANT: Ferguson, Kenneth M.
APPLICANT: Francis, Sharron H.
APPLICANT: Kadlecek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,547A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5652131and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32791
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-547A-10

Query Match 38.6%; Score 1355.5; DB 1; Length 875;
Best Local Similarity 42.9%; Pred. No. 6e-119;
Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTSLLCMPIRSSDGLIIGVQAQAIN-KIPGAPFTDEDEKVMQMY 112
Db 54 KDRFNDEIDKLTGYKTSLLCMPIRSSDGLIIGVQAQAIN-KIPGAPFTDEDEKVMQMY 112
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Db 237 EDPREAEVDQITGYKTKSILCMPIKHNREVVGVQAQAINKKSGNGGTFTEKDEKDFAA 296
QY 113 LPFCGIAISNAQFAASRKEYERSRALLEVNDLFEQTDLEKIVKIMHRAQTLLKGER 172
Db 297 LAFCGIVLHNAQLYETSLENKRNQVLLDLASLIFEEOQSLEVLKKAATIIISFMQVOK 356
QY 173 CSVLLLEDIESPVVKFTKSFELMSPKCSADASENFK-----ESMEKSSYSDDL----- 220
Db 357 CTITFVDE-----DCSDSFSFVHMECELEKS--SDTLTRERD 393
QY 221 ---INNSIAELVASTGLPVNLSDAVQDPRFADAEADQISGFH---IRSVLCVPIWN-SHQ 273
Db 394 ANRINYVAQVYKNTMEPLNIPDVSKRFPWTNENMGNIQOCCIRSLCTPIKNGKKN 453
QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVFCGLGINNTIYDOVKKSWAKQSVAL 328
Db 454 VIGVCQLVNMKEETGKVKAFNRNDEQFLFAFVFCGLGIQNTQMYEAVRAMAKQMTL 513
QY 329 DVLSYHATCSK---AEVDKFKAAANIPLVSELAIDDIHFDDFSVDAMITAAALRMFELG 385
Db 514 EVLSYHASAAEETRELQSLAAAVVPSAQTLLKITDIFSDFSELSDELTALETCTIRMFTDLN 573
QY 386 MVQFKIDYETLCRWLLTVRKNYRM-VLYHNHRAFNVCOLMFAMLTTAGFQDILTEVEI 444
Db 574 LVQNFQMKHEVLCRWLLSVKKNYRNKRNVAHNHRAFNVAQCMFAALKAGKIQKRLTDLEI 633
QY 445 LAVIVGCLCHDLDRGTNNAFQAKSGSALAQLYGTSALEHHHFNHVAVMILQSEGHNTFA 504
Db 634 LALLIAALSHDLDRGVNNSYQIORSHEPLAQLY-CHSIMEHHHFDQCLMILNSPGNQILS 692
QY 505 NLSKEYSDMLQKSLATDLTYLFERRTEFFELVSKGYEDWNKINHRDIFRSMMLTA 564
Db 693 GLSIEYKTKLIIKQAILATDLALYIKRRGEFFELIMKNQFNLEDPHQKELFLAMLMTA 752
QY 565 CDLGAVTKPWEISROVAELVSEFEQDGRERLELKTPTSAIFDRNRKDELPRLOLEWID 624
Db 753 CDLSAITKPMPIQOIRIAELVATEFFDQGRERKELNIEPADLMNREKKNKIPSMQVGFID 812
QY 625 SICMPLYQALYKVNKLPMLDSVATNRSKWEEL--HOKRLLASTASSSS 672
Db 813 AICQLQYALTHVSEDCFPLLDGCGRKNQKQWALAEQOEKTLINGESSQT 862

RESULT 13

US-08-250-847B-10

Sequence 10, Application US/08250847B

Patent No. 5702936

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.

APPLICANT: Corbin, Jackie D.

APPLICANT: Ferguson, Kenneth M.

APPLICANT: Francis, Sharon H.

APPLICANT: Kadlec, Ann

APPLICANT: Loughney, Kate

APPLICANT: McAllister-Lucas, Linda M.

APPLICANT: Sonnenburg, William K.

APPLICANT: Thomas, Melissa K.

TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific

TITLE OF INVENTION: Phosphodiesterase Materials and Methods

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/250-847B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5702936and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
* TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-250-847B-10

Query Match 38.6%; Score 1355.5; DB 1; Length 875;

Best Local Similarity 42.9%; Pred. No. 6e-119;

Matches 279; Conservative 129; Mismatches 187; Indels 55; Gaps 12;

QY 54 KDRFNDEIDKLTGYKTKSLLCMPIRSDGFIIGVAQAIN-KIPEGAPFTEDEKVMOMY 112

Db 237 EDPREAEVDQITGYKTKSILCMPIKHNREVVGVQAQAINKKSGNGGTFTEKDEKDFAA 296

QY 113 LPFCGIAISNAQFAASRKEYERSRALLEVNDLFEQTDLEKIVKIMHRAQTLLKGER 172

Db 297 LAFCGIVLHNAQLYETSLENKRNQVLLDLASLIFEEOQSLEVLKKAATIIISFMQVOK 356

QY 173 CSVLLLEDIESPVVKFTKSFELMSPKCSADASENFK-----ESMEKSSYSDDL----- 220

Db 357 CTITFVDE-----DCSDSFSFVHMECELEKS--SDTLTRERD 393

QY 221 ---INNSIAELVASTGLPVNLSDAVQDPRFADAEADQISGFH---IRSVLCVPIWN-SHQ 273

Db 394 ANRINYVAQVYKNTMEPLNIPDVSKRFPWTNENMGNIQOCCIRSLCTPIKNGKKN 453

QY 274 IIGVAQVNLRLDG-----KPFDDADQRLFEAFVFCGLGINNTIYDOVKKSWAKQSVAL 328

Db 454 VIGVCQLVNMKEETGKVKAFNRNDEQFLFAFVFCGLGIQNTQMYEAVRAMAKQMTL 513

QY 329 DVLSYHATCSK---AEVDKFKAAANIPLVSELAIDDIHFDDFSVDAMITAAALRMFELG 385

Db 514 EVLSYHASAAEETRELQSLAAAVVPSAQTLLKITDIFSDFSELSDELTALETCTIRMFTDLN 573

QY 386 MVQFKIDYETLCRWLLTVRKNYRM-VLYHNHRAFNVCOLMFAMLTTAGFQDILTEVEI 444

Db 574 LVQNFQMKHEVLCRWLLSVKKNYRNKRNVAHNHRAFNVAQCMFAALKAGKIQKRLTDLEI 633

QY 445 LAVIVGCLCHDLDRGTNNAFQAKSGSALAQLYGTSALEHHHFNHVAVMILQSEGHNTFA 504

Db 634 LALLIAALSHDLDRGVNNSYQIORSHEPLAQLY-CHSIMEHHHFDQCLMILNSPGNQILS 692

QY 505 NLSKEYSDMLQKSLATDLTYLFERRTEFFELVSKGYEDWNKINHRDIFRSMMLTA 564

Db 693 GLSIEYKTKLIIKQAILATDLALYIKRRGEFFELIMKNQFNLEDPHQKELFLAMLMTA 752

QY 565 CDLGAVTKPWEISROVAELVSEFEQDGRERLELKTPTSAIFDRNRKDELPRLOLEWID 624

Db 753 CDLSAITKPMPIQOIRIAELVATEFFDQGRERKELNIEPADLMNREKKNKIPSMQVGFID 812

QY 625 SICMPLYQALYKVNKLPMLDSVATNRSKWEEL--HOKRLLASTASSSS 672

Db 813 AICQLQYALTHVSEDCFPLLDGCGRKNQKQWALAEQOEKTLINGESSQT 862

RESULT 14

US-08-463-949A-10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:09 ; Search time 58.4282 seconds
(without alignments)
1559.921 Million cell updates/sec

Title: US-09-663-542-1
Perfect score: 3516
Sequence: 1 MLKQRRPLFRNLSATQWK.....ASTASSSPASVMWAKEDRN 684

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3516	100.0	684	22 AAG62678	Human type 11 phos
2	3516	100.0	684	22 AAB35472	Human cyclic nucle
3	3294.5	93.7	685	22 AAG62679	Rat type 11 phosph
4	3250	92.4	934	22 AAG62677	Human type 11 phos
5	3117.5	88.7	935	22 AAG62680	Rat type 11 phosph
6	2970	84.5	576	22 AAG67533	Amino acid sequenc
7	2541	72.3	490	21 AAY95521	Human cyclic nucle
8	2458	69.9	474	22 AAG67531	Amino acid sequenc
9	1762	50.1	367	21 AAY95522	Human cyclic nucle
10	1511.5	43.0	1284	22 ABB71869	Drosophila melanog

11	1511.5	43.0	1284	23 ABB08376	D. melanogaster CG
12	1380.5	39.3	1232	22 ABB63685	Drosophila melanog
13	1374	39.1	1126	21 AAY84879	Amino acid sequenc
14	1366.5	38.9	832	21 AAY78940	Human phosphodiester
15	1366.5	38.9	833	21 AAY90912	Human cGMP phospho
16	1366.5	38.9	833	22 AAB97024	Human phosphodiester
17	1366.5	38.9	875	16 AAR66565	Cyclic guanosine m
18	1366.5	38.9	875	20 AAY14991	Human cGMP-binding
19	1359.5	38.7	832	21 AAY78939	Human phosphodiester
20	1355.5	38.6	875	19 AAW42011	Bovine cGMP-bindin
21	1355.5	38.6	875	20 AAV14990	Bovine cGMP-bindin
22	1349.5	38.4	875	16 AAR66564	Cyclic guanosine m
23	956	27.2	789	21 AAY53935	A human phosphodie
24	956	27.2	791	21 AAY53936	A human phosphodie
25	951	27.0	766	20 AAY13934	Human phosphodiester
26	951	27.0	766	22 AAB28256	Human phosphodiester
27	951	27.0	803	20 AAV13935	Human phosphodiester
28	951	27.0	803	22 AAB28257	Human phosphodiester
29	950	27.0	779	20 AAY13936	Human phosphodiester
30	950	27.0	779	21 AAB28653	Human phosphodiester
31	950	27.0	779	22 AAB73486	Human cyclic nucle
32	950	27.0	779	22 AAB28258	Human phosphodiester
33	950	27.0	789	21 AAB26854	Human phosphodiester
34	949	27.0	806	22 AAM51617	Human PDE10A polyp
35	934.5	26.6	941	16 AAR69729	Cyclic-GMP stimula
36	934.5	26.6	941	18 AAM18050	Human cGS-PDE amin
37	934.5	26.6	941	18 AAM11253	pHcgs6n cyclic GMP
38	934.5	26.6	941	19 AAW77042	Cyclic-GMP-stimula
39	934.5	26.6	941	19 AAW71226	Human cGS-PDE CDNA
40	934.5	26.6	941	19 AAW60754	Human cyclic-GMP-n
41	934.5	26.6	941	21 AAY80986	Human cGS-PDE, SEQ
42	934.5	26.6	941	22 AAE07918	Human phosphodiester
43	934.5	26.6	941	22 AAE07954	Human phosphodiester
44	934.5	26.6	941	22 AAG66539	Human interferon-a
45	934.5	26.6	941	22 AAB85106	Human cGMP-stimula

ALIGNMENTS

RESULT 1
AAG62678
ID AAG62678 standard; Protein: 684 AA.
XX
AC AAG62678;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human type 11 phosphodiesterase SEQ ID NO: 4.
XX
KW Human; type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.
XX
OS Homo sapiens.
XX
PN WO200146436-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-JP09118.
XX
PR 22-DEC-1999; 99Jp-0364866.
PR 01-JUN-2000; 2000JP-0163875.
XX
(TANA) TANABE SEIYAKU CO.
XX
PI Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX
DR WPI: 2001-418074/44.
XX
DR N-PSDB; AA466709.
XX
PT Type 11 phosphodiesterases and encoded genes with activity of
hydrolyzing cyclic nucleotides, useful for studying intracellular

PT signal transduction mechanism and in screening highly-selective
XX inhibitors as drugs with superior efficacy
PS
XX
XX
XX

Claim 2; Page 49-51; 77pp; Japanese.

CC The present invention provides the protein and coding sequences of novel
CC human and rat type II phosphodiesterases (PDEII). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX Sequence 684 AA;

Query Match 100.0%; Score 3516; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.3e-304;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAERKQKHQDFLIQROTQTKDRRND 60
DB 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAERKQKHQDFLIQROTQTKDRRND 60

QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
DB 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120

QY 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180
DB 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180

QY 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240
DB 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240

QY 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGKPFDDADQRLFEAF 300
DB 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGKPFDDADQRLFEAF 300

QY 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
DB 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360

QY 361 IHFDDFSLLDAMDITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420
DB 361 IHFDDFSLLDAMDITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420

QY 421 NYCQLMFAMLTAGQDILTEVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAQLYGTG 480
DB 421 NYCQLMFAMLTAGQDILTEVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAQLYGTG 480

QY 481 ATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLYFERRTEFFEL 540
DB 481 ATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLYFERRTEFFEL 540

QY 541 VSKGEYDNWIKNHRDIFRSMILMTACDLGAVTKPWEISQVAVELTSEFFEQDRLRLK 600
DB 541 VSKGEYDNWIKNHRDIFRSMILMTACDLGAVTKPWEISQVAVELTSEFFEQDRLRLK 600

QY 601 LTPSAIFDRNRKDELPRLOLEWIDISICMPLVQALYKVNKLPMLDSVATNRKSWHEELHQ 660
DB 601 LTPSAIFDRNRKDELPRLOLEWIDISICMPLVQALYKVNKLPMLDSVATNRKSWHEELHQ 660

QY 661 KRLLASTASSSSPASVMVAKEDRN 684
DB 661 KRLLASTASSSSPASVMVAKEDRN 684

RESULT 2
AAB35472
ID AAB35472 standard; protein; 684 AA.
XX
AC AAB35472;

XX 06-JUN-2001 (first entry)
XX Human cyclic nucleotide phosphodiesterase PDEXV.
DE
XX
XX Human cyclic nucleotide phosphodiesterase; PDEXV; sexual dysfunction;
KW cardiovascular disease; gastrointestinal disorder; corpus cavernosum;
KW kidney; liver; skeletal muscle; testis prostate; spleen.
XX
XX Homo sapiens.
OS
XX
XX EP1085089-A2.
PN
XX
XX 21-MAR-2001.
PD
XX
XX 14-SEP-2000; 2000EP-0307981.
PF
XX
XX 17-SEP-1999; 99GB-0022124.
PR
XX
XX (PFIZ) PFIZER LTD.
PA
XX (PFIZ) PFIZER INC.
PA
XX
PI Fidock MD, Robas NM;
DR
XX WPI: 2001-246900/26.
DR N-PSDB; AAF62311.
XX
XX Human cyclic nucleotide phosphodiesterase and its nucleotide sequence
PT useful for treating cardiovascular disorders, sexual dysfunction and
PT screening for drugs to treat associated disorders -
XX
XX Claim 1; Page 37-41; 44pp; English.
PS
XX
XX The present invention describes the protein and coding sequences of the
CC human cyclic nucleotide phosphodiesterase PDEXV. This enzyme is capable
CC of catalysing the degradation of cyclic nucleotides. The sequences are
CC useful in the treatment of cardiovascular, gastrointestinal, spleen,
CC corpus cavernosum, kidney, liver, skeletal muscle, testis and prostate
CC related disorders, and in the enhancement of the male erectile response
CC and the treatment of female sexual dysfunction. The present sequence is
CC the PDEXV protein.
XX
SQ Sequence 684 AA;

Query Match 100.0%; Score 3516; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.3e-304;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAERKQKHQDFLIQROTQTKDRRND 60
DB 1 MLKQARRPLFRNVLSTATQWKKVITRLVQISGASLAERKQKHQDFLIQROTQTKDRRND 60

QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
DB 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120

QY 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180
DB 121 SNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKERCSCVLLLED 180

QY 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240
DB 181 IESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLNINNSIAELVASTGLPVTSD 240

QY 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGKPFDDADQRLFEAF 300
DB 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGKPFDDADQRLFEAF 300

QY 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
DB 301 VIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360

QY 361 IHFDDFSLLDAMDITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420
DB 361 IHFDDFSLLDAMDITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNWRHAF 420

QY 421 NYCQLMFAMLTAGQDILTEVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAQLYGTG 480
DB 421 NYCQLMFAMLTAGQDILTEVEILAVIVGCLCHDLHRGTNNAFQAKSGSALAQLYGTG 480

QY 481 ATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLYFERRTEFFEL 540
DB 481 ATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLYFERRTEFFEL 540

QY 541 VSKGEYDNWIKNHRDIFRSMILMTACDLGAVTKPWEISQVAVELTSEFFEQDRLRLK 600
DB 541 VSKGEYDNWIKNHRDIFRSMILMTACDLGAVTKPWEISQVAVELTSEFFEQDRLRLK 600

QY 601 LTPSAIFDRNRKDELPRLOLEWIDISICMPLVQALYKVNKLPMLDSVATNRKSWHEELHQ 660
DB 601 LTPSAIFDRNRKDELPRLOLEWIDISICMPLVQALYKVNKLPMLDSVATNRKSWHEELHQ 660

QY 661 KRLLASTASSSSPASVMVAKEDRN 684
DB 661 KRLLASTASSSSPASVMVAKEDRN 684

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Db 361 IHFDDFSLVDVDMITAAALRMFMELGMVQFKIDYETLCRWLLTVRKMYRMVLYNHRHAF 420
QY 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFOAKSGSALAQLYGTG 480
Db 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFOAKSGSALAQLYGTG 480
QY 481 ATLEHHFHNHVMILQSEGHNIIFANLSSKEYSDLMQLLKQSILATDLYFERTTEFFEL 540
Db 481 ATLEHHFHNHVMILQSEGHNIIFANLSSKEYSDLMQLLKQSILATDLYFERTTEFFEL 540
QY 541 VSKGEYDWNKKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600
Db 541 VSKGEYDWNKKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600
QY 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKVNVKLPMLDSVATNRKSWHEELHQ 660
Db 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKVNVKLPMLDSVATNRKSWHEELHQ 660
QY 661 KRLLASTASSSSPASVWVAKEDRN 684
Db 661 KRLLASTASSSSPASVWVAKEDRN 684

```

RESULT 3

AAG62679 standard; Protein: 685 AA.

AC AAG62679;

DT 19-SEP-2001 (first entry)

DE Rat type 11 phosphodiesterase SEQ ID NO: 6.

KW Rat; type 11 phosphodiesterase; PDE11; signal transduction;

XX selective inhibition.

OS Rattus sp.

XX WO200146436-A1.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-JP09118.

XX 22-DEC-1999; 99JP-0364866.

XX 01-JUN-2000; 2000JP-0163875.

XX (TANA) TANABE SEIYAKU CO.

XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX WPI: 2001-418074/44.

XX N-PSDB; AAH46710.

XX Type 11 phosphodiesterases and encoded genes with activity of

PT hydrolyzing cyclic nucleotides, useful for studying intracellular

PT signal transduction mechanism and in screening highly-selective

PT inhibitors as drugs with superior efficacy

XX Claim 2; Page 55-57; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel

CC human and rat type 11 phosphodiesterases (PDE11). These are useful for

CC studying intracellular signal transduction mechanisms, in screening

CC highly-selective inhibitors as drugs for treating diseases associated

CC with the enzymes and for the identification or selection of selective

CC inhibitory action against multiple type phosphodiesterases. The present

CC sequence is a protein of the invention.

XX Sequence 685 AA;

SQ Query Match 93.7%; Score 3294.5; DB 22; Length 685;

```

Best Local Similarity 93.7%; Pred. No. 7.9e-285;
Matches 644; Conservative 13; Mismatches 23; Indels 7; Gaps 2;

QY 1 MLKQARPLFRNVLSATQWKKVKITRLVQLSGSLAEKOEKHQDFLQROTTKDRRFND 60
Db 1 MLKQARPLFRNVLSATQWKKVKITRLVQLSGSLAEKOEKHQDFLQROTTKDRRFND 60

QY 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMLPFCGIAI 120
Db 61 EIDKLTGYKTKSLLCMPIRNSDGEIIGVAQAINKVPEGAPFTEDEKVMQMLPFCGIAI 120

QY 121 SNAQLFAASKEYERSRALLEVVNDLFEQTDLEKIVKKIMHRAQTLLKERCSSLLED 180
Db 121 SNAQLFAASKEYERSRALLEVVNDLFEQTDLEKIVKKIMHRAQTLLKERCSSLLED 180

QY 181 IESPVVKFTKSFELMSPKCSADAENSEKSWKSSYSDWLNINSIAELVASTGLPVNISD 240
Db 181 IESPVVKFTKSFELMSPKCSADAENSEKSWKSSYSDWLNINSIAELVASTGLPVNISD 240

QY 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLNLDGKPFDDADQRLFEAF 300
Db 241 AYQDPRFDEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLNLDGKPFDDADQRLFEAF 300

QY 301 VIFCGLGINTIMYDQVKKSWAKQSVADLVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360
Db 301 VIFCGLGINTIMYDQVKKSWAKQSVADLVLSYHATCSKAEDVKFKAANIPLVSELAIDD 360

QY 361 IHFDDFSLVDVDMITAAALRMFMELGMVQFKIDYETLCRWLLTVRKMYRMVLYNHRHAF 420
Db 361 IHFDDFSLVDVDMITAAALRMFMELGMVQFKIDYETLCRWLLTVRKMYRMVLYNHRHAF 420

QY 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFOAKSGSALAQLYGTG 480
Db 421 NVCOLMFAMLTITAGFODILTEVEILAVIVGCLCHDHRGTNNAFOAKSGSALAQLYGTG 480

QY 481 ATLEHHFHNHVMILQSEGHNIIFANLSSKEYSDLMQLLKQSILATDLYFERTTEFFEL 540
Db 481 ATLEHHFHNHVMILQSEGHNIIFANLSSKEYSDLMQLLKQSILATDLYFERTTEFFEL 540

QY 541 VSKGEYDWNKKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600
Db 541 VSKGEYDWNKKNHRDIFRSMMLTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELK 600

QY 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKVNVKLPMLDSVATNRKSWHEELHQ 660
Db 601 LTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKVNVKLPMLDSVATNRKSWHEELHQ 660

QY 661 KRLLASTA-----SSSSPASVWVAKEDR 683
Db 661 KRLLASTA-----SSSSPASVWVAKEDR 684

```

RESULT 4

AAG62677 standard; Protein: 934 AA.

AC AAG62677;

DT 19-SEP-2001 (first entry)

DE Human type 11 phosphodiesterase SEQ ID NO: 2.

XX Human; type 11 phosphodiesterase; PDE11; signal transduction;

XX selective inhibition.

XX Homo sapiens.

XX WO200146436-A1.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-JP09118.

XX

PR 22-DEC-1999; 99JP-0364866.
XX 01-JUN-2000; 2000JP-0163875.
PA (TANA) TANABE SEIYAKU CO.
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX WPI; 2001-418074/44.
DR N-PSDB; AAH46708.
XX
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy
XX
XX Claim 2; Page 42-45; 77pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.
XX
SQ Sequence 934 AA;
Query Match 92.4%; Score 3250; DB 22; Length 934;
Best Local Similarity 99.8%; Pred. No. 1.2e-280;
Matches 630; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 54 KDRFNDEIDKLGKTKSLLCMPIRSSDGEIIGVAAQAINKIPEGAPFTEDEKVMQMYL 113
DB :|||||
DB 304 QDRFNDEIDKLGKTKSLLCMPIRSSDGEIIGVAAQAINKIPEGAPFTEDEKVMQMYL 363
QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFESQTDLEKIVKKIMHRAQTLLKCERC 173
DB :|||||
DB 364 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFESQTDLEKIVKKIMHRAQTLLKCERC 423
QY 174 SVLLEDIESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLIINNSIAELVASTG 233
DB :|||||
DB 424 SVLLEDIESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLIINNSIAELVASTG 483
QY 234 LPVNISDAYQDPFDEADQISGFHRSVLCVPIWNSHQIIGVAAQVLRDLGKPPDDAD 293
DB :|||||
DB 484 LPVNISDAYQDPFDEADQISGFHRSVLCVPIWNSHQIIGVAAQVLRDLGKPPDDAD 543
QY 294 QRLFEAFVIFCGLGINTIMYDOVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLV 353
DB :|||||
DB 544 QRLFEAFVIFCGLGINTIMYDOVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLV 603
QY 354 SELAIDDIHFDLDFSLDVAIMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 413
DB :|||||
DB 604 SELAIDDIHFDLDFSLDVAIMITAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLY 663
QY 414 HNRHAFNVCQLMFAMLTITAGFODILTEVEILLAVIVGCLCHDLDRGTNNAFQKSGSAL 473
DB :|||||
DB 664 HNRHAFNVCQLMFAMLTITAGFODILTEVEILLAVIVGCLCHDLDRGTNNAFQKSGSAL 723
QY 474 AQLYGTSAILEHHFHNHAWILOSSEGHNTFANLSKEYSDLMQLLKQSLATDLTYLPER 533
DB :|||||
DB 724 AQLYGTSAILEHHFHNHAWILOSSEGHNTFANLSKEYSDLMQLLKQSLATDLTYLPER 783
QY 534 RTEFFELVSKGEYDWNKIHNRDIFRSMLTACDLGAVTKPWELSRVAELVTSERFEQGD 593
DB :|||||
DB 784 RTEFFELVSKGEYDWNKIHNRDIFRSMLTACDLGAVTKPWELSRVAELVTSERFEQGD 843
QY 594 RERLEKLTPTSAIFDRNRKDELPRLOLEWIDSTCMPLYQALVKVNVKLPMLDSVATNRS 653
DB :|||||
DB 844 RERLEKLTPTSAIFDRNRKDELPRLOLEWIDSTCMPLYQALVKVNVKLPMLDSVATNRS 903
QY 654 KWELHOKRLLASTASSSSPASVWAKEDRN 684
DB :|||||

DB 904 KWELHOKRLLASTASSSSPASVWAKEDRN 934
RESULT 5
AAG62680
ID AAG62680 standard; Protein; 935 AA.
XX
XX AAG62680;
XX
XX 19-SEP-2001 (first entry)
XX
XX Rat type 11 phosphodiesterase SEQ ID NO: 39.
DE
XX Rat; type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.
XX
XX Rattus sp.
OS
XX WO200146436-A1.
PN
XX
XX 28-JUN-2001.
PD
XX
XX 22-DEC-2000; 2000WO-JP09118.
PF
XX
XX 22-DEC-1999; 99JP-0364866.
PR
XX 01-JUN-2000; 2000JP-0163875.
PR
XX (TANA) TANABE SEIYAKU CO.
PA
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
XX
XX WPI; 2001-418074/44.
DR
XX N-PSDB; AAH46742.
DR
XX
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy
XX
XX Claim 2; Page 69-72; 77pp; Japanese.
PS
XX
XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.
XX
SQ Sequence 935 AA;
Query Match 88.7%; Score 3117.5; DB 22; Length 935;
Best Local Similarity 95.6%; Pred. No. 7.8e-269;
Matches 606; Conservative 9; Mismatches 12; Indels 7; Gaps 2;
QY 54 KDRFNDEIDKLGKTKSLLCMPIRSSDGEIIGVAAQAINKIPEGAPFTEDEKVMQMYL 113
DB :|||||
DB 304 QDRFNDEIDKLGKTKSLLCMPIRSSDGEIIGVAAQAINKIPEGAPFTEDEKVMQMYL 363
QY 114 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFESQTDLEKIVKKIMHRAQTLLKCERC 173
DB :|||||
DB 364 PFCGIAISNAQLFAASRKEYERSRALLEVVNDLFESQTDLEKIVKKIMHRAQTLLKCERC 423
QY 174 SVLLEDIESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLIINNSIAELVASTG 233
DB :|||||
DB 424 SVLLEDIESPVVKFTKSFELMSPKCSADAENSKESMEKSSYSDWLIINNSIAELVASTG 483
QY 234 LPVNISDAYQDPFDEADQISGFHRSVLCVPIWNSHQIIGVAAQVLRDLGKPPDDAD 293
DB :|||||
DB 484 LPVNISDAYQDPFDEADQISGFHRSVLCVPIWNSHQIIGVAAQVLRDLGKPPDDAD 543
QY 294 QRLFEAFVIFCGLGINTIMYDOVKKSWAKQSVLDVLSYHATCSKAEDVKFKAANIPLV 353
DB :|||||

Db 544 ORLFAFVIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAANIPLV 603
QY 354 SELAIDDIHFDDFSVDVAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNNRMVLY 413
Db 604 SELAIDDIHFDDFSVDVAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNNRMVLY 663
QY 414 HNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAKSGSAL 473
Db 664 HNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAKSGSAL 723
QY 474 AOLYGTSAATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLTLTYFER 533
Db 724 AOLYGTSAATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLTLTYFER 783
QY 534 RTEFFELVSKGEYDWNINRHRDIFRSMELMTACDLGAVTKPWEISRQVAELVTSEFQEGD 593
Db 784 RTEFFELVSKGAYDWSITSHRDVFRSMLMTACDLGAVTKPWEISRQVAELVTSEFQEGD 843
QY 594 RERLEKLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVNAKLKPMLDSDVATNRS 653
Db 844 RERSELKTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVNAKLKPMLDSDVATNRS 903
QY 654 KWEELHQRRLASTA---SSSSPASVMVAKEDR 683
Db 904 KWEELHQRRLQVSAASPVSPSPA---VAGEDR 934

RESULT 6
AAG67533
ID AAG67533 standard; Protein; 576 AA.
XX
AC AAG67533;
DT
XT
XX 26-NOV-2001 (first entry)
DE Amino acid sequence of a human phosphodiesterase polypeptide.
XX Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;
KW nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;
KW osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;
KW Parkinson's disease; dementia; infectious disease; malignant tumour.
XX
OS Homo sapiens.
XX
XX WO200166716-A1.
XX
XX 13-SEP-2001.
PP 06-MAR-2001; 2001WO-JP01720.
XX
XX 07-MAR-2000; 2000JP-0061464.
PR 10-JUL-2000; 2000JP-0208610.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Miyaaji H, Haruoka M, Ota T, Kawabata A, Sugano S, Nakamura Y;
PI WPI; 2001-570769/64.
XX
DR N-PSDB; AAH78232.
DR
XX Polypeptides with phosphodiesterase activity and DNA for treatment of
PT diabetes, ischemic heart disease, hypertension, nephritis,
PT pancreatitis, ulcers, allergies, asthma
XX
XX Claim 1; Page 90-93; 105pp; Japanese.
XX
CC The present sequence encodes a human polypeptide which has
CC phosphodiesterase activity. The phosphodiesterase polypeptide and
CC polynucleotide are used for the treatment and prevention of diabetes,
CC ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers,
CC allergies, asthma, rheumatism, osteoporosis, pain, anxiety,
CC schizophrenia, manic depressive psychosis, Parkinson's disease,
CC dementia, infectious diseases, and malignant tumours.
XX

XX Sequence 576 AA;
SQ
Query Match 84.5%; Score 2970; DB 22; Length 576;
Best Local Similarity 100.0%; Pred. No. 5.4e-256;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 MQMYPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLL 168
Db 1 MQMYPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKKIMHRAQTLL 60
QY 169 KCERCSVLLLEDDIESPVVKFTKSFELMSPKCSADAENESFKESMEKSSYSDWLNNISIAL 228
Db 61 KCERCSVLLLEDDIESPVVKFTKSFELMSPKCSADAENESFKESMEKSSYSDWLNNISIAL 120
QY 229 VASTGLPVNISDAYODPRFDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGRP 288
Db 121 VASTGLPVNISDAYODPRFDAEADQISGFHRSVLCVPIWNSNHQIIGVAQVNLRLDGRP 180
QY 289 FDDAQRLFEAFVIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAA 348
Db 181 FDDAQRLFEAFVIFCGLGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEDVKFAA 240
QY 349 NIPLVSELAIDDIHFDDFSVDVAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNN 408
Db 241 NIPLVSELAIDDIHFDDFSVDVAMITAAALRMFMELGMVQKFKIDYETLCRWLLTVRKNN 300
QY 409 RMVLYHNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAK 468
Db 301 RMVLYHNRHAFNVQCMFAMLTAGFQDILTEVEILAVIGCLCHDLDRGTNNAFQAK 360
QY 469 SGSALAQLYGTSAATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLT 528
Db 361 SGSALAQLYGTSAATLEHHHFNHVMILQSEGHNFANLSKEYSDLMQLLKQSLATDLT 420
QY 529 LYFERTEFFELVSKGEYDWNINRHRDIFRSMELMTACDLGAVTKPWEISRQVAELVTSEF 588
Db 421 LYFERTEFFELVSKGEYDWNINRHRDIFRSMELMTACDLGAVTKPWEISRQVAELVTSEF 480
QY 589 FEQGRERLEKLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVNAKLKPMLDSDV 648
Db 481 FEQGRERLEKLTPSAIFDRNRKDELPRQLQLEWIDSCIMPLYQALVKNVNAKLKPMLDSDV 540
QY 649 ATNRSKWEELHQRRLASTASSSSPASVMVAKEDRN 684
Db 541 ATNRSKWEELHQRRLASTASSSSPASVMVAKEDRN 576
RESULT 7
AAY95521
ID AAY95521 standard; Protein; 490 AA.
XX
AC AAY95521;
XX
DT 10-OCT-2000 (first entry)
XX
XX Human cyclic nucleotide phosphodiesterase HSPDE10A1.
DE
XX Cyclic nucleotide phosphodiesterase; HSPDE10A1; human; cancer;
KW immune disorder; diagnosis; therapy.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH 196..458
FT /note= "catalytic domain"
FT 88..99
FT /note= "putative cGMP binding motif"
FT 260..269
FT /note= "phosphodiesterase signature motif"
XX
XX WO200040733-A1.
XX

Db 301 YSDLMQLLKQSLATDLTLYFERRTEFFELVSKGEYDWNKIHNRDIFRMLMTACDLGAV 360
QY 571 TKPWEISQVLAELVTSFEFFQDRELRLEKLTSPSIFDRNRKDELPRQLQLEWIDSICMPL 630
Db 361 TKPWEISQVLAELVTSFEFFQDRELRLEKLTSPSIFDRNRKDELPRQLQLEWIDSICMPL 420
QY 631 YOALVKVNVKLPMLDSVATNRKSWHEELHQRLRLASTASSSSPASVMVAKEDRN 684
Db 421 YOALVKVNVKLPMLDSVATNRKSWHEELHQRLRLASTASSSSPASVMVAKEDRN 474

RESULT 9
ID AAY95522 standard; Protein; 367 AA.
XX
AC AAY95522;
XX
DT 10-OCT-2000 (first entry)
XX
DE Human cyclic nucleotide phosphodiesterase HSPDE10A2.
KW Cyclic nucleotide phosphodiesterase; HSPDE10A2; human; cancer;
KW immune disorder; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 88..99
FT /note= "putative cGMP binding motif"
FT Peptide 260..269
FT /note= "phosphodiesterase signature motif"
XX
XX WO200040733-A1.
PN 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00371.
PR
XX 07-JAN-1999; 99US-0226741.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Phillips SC, Lanfear J, Fawcett L, Bandman O, Harrow I;
XX
XX WPI; 2000-452539/39.
DR N-PSDB; AAA49973.
XX
XX New human cyclic nucleotide phosphodiesterases, referred as HSPDE10A1
PT and HSPDE10A2, useful for treating and preventing cancer and immune
PT disorders -
XX
XX Claim 1; Page 84; 96pp; English.
PS
XX
CC The present sequence is that of HSPDE10A2, a novel human cyclic
CC nucleotide phosphodiesterase. The amino acid sequence was deduced
CC from an isolated cDNA clone (see AAA49973). HSPDE10A2 is a
CC C-terminal splice variant of HSPDE10A1 (see AAY95521), being
CC identical between amino acid residues 1-338, but different in the
CC C-terminal portion from residue 339 to 367. It shares 40%
CC identity with HSPDE3A1. The invention provides expression vectors,
CC host cells, antibodies, agonists and antagonists, as well as
CC methods for diagnosing, treating or preventing disorders associated
CC with expression of HSPDE10A1, especially cancer and immune
CC disorders.
XX
SQ Sequence 367 AA;

Query Match 50.1%; Score 1762; DB 21; Length 367;
Best Local Similarity 99.4%; Pred. No. 1.7e-148;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 195 MSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDEADQI 254
|||||

Db 1 MSPKCSADAENSFKESMEKSSYSDWLINNSIAELVASTGLPVNISDAYQDPRFDEADQI 60
QY 255 SGFHRSVLCVPIMWSNHQIIGVAOVNLNLDCKPDDADQRLFEAFVIFCGIGINNNTIMY 314
Db 61 SGFHRSVLCVPIMWSNHQIIGVAOVNLNLDCKPDDADQRLFEAFVIFCGIGINNNTIMY 120
QY 315 DQVKKSWAKQSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDDIHFDDFSLOVDAMI 374
Db 121 DQVKKSWAKQSVALDVLSYHATCSKAEDVKFKAANIPLVSELAIDDIHFDDFSLOVDAMI 180
QY 375 TAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFAMLTAG 434
Db 181 TAALRMFMELGMVQKFKIDYETLCRWLLTVRKNYRMVLYHNHRHAFNVQCLMFAMLTAG 240
QY 435 FODILTEVEILAVIVGCLCHDLHRTGNNAFQKSGSALAQLYGTSALEHHHFNHAVMI 494
Db 241 FODILTEVEILAVIVGCLCHDLHRTGNNAFQKSGSALAQLYGTSALEHHHFNHAVMI 300
QY 495 LQSEGHNIFANLSKESYSDLMQLLKQSLATDLTLYFERR 534
Db 301 LQSEGHNIFANLSKESYSDLMQLLKQSLATDLTLYFERR 340

RESULT 10
ID ABB71869 standard; Protein; 1284 AA.
XX
AC ABB71869;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 42399.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
PA
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL15972.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 42399; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1284 AA;

Db 676 LCRWLLSVKKNVYNNVYHNHAFNVAOMFAILLTTOHWKIFGEIECLALIGCLCHDL 735
 QY 457 DHRGTNAPQAKSGSALAQLYGTSAFLEHHHFNHAWMILOQSEGHNFANLSKEYSCLMQ 516
 Db 736 DHRGTNNSQIKASSPLAQLYSTS-TMEHHHFDQCLMILNSFGNQILANLSSDDYCRVIR 794
 QY 517 LKQSTILATDLILYFERRTEFFELVSKGYDNNKHNHRDIFRSMLMTACDLGAVTKPWEI 576
 Db 795 VLEDAILSTDLAVYFKKGPFLSVSQPTSYVVAEPRALLRAMSMTVCDSLTAITKPWEI 854
 QY 577 SRQVAELVTSSEFEQDGERLEKLTPSAIFDRNRKDELPRLOLEWIDSICMPLYQALVK 636
 Db 855 ERKRVADLVSEFEQDGMKEQLNIITPIDIMNREKEDELPMQVNFIDSICLPVEAFAT 914
 QY 637 VNVKLPMLDSVATNRSKWEEL 658
 Db 915 LSDKLEPLVEGVDRNRGHWIDL 936

RESULT 12

ABB63685
 ID ABB63685 standard; Protein; 1232 AA.

AC ABB63685;

XX 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 17847.

DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL07788.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions

XX Disclosure; SEQ ID NO 17847; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1232 AA;

Query Match 39.3%; Score 1380.5; DB 22; Length 1232;
 Best Local Similarity 38.9%; Pred. No. 1.le-113;
 Matches 299; Conservative 109; Mismatches 211; Indels 149; Gaps 10;

QY 28 VOISGASLAEOEKHODFIQROTQTKDRRNFENDEIDKLTGYTKTSLCIMPISDSGEIIG 87
 Db 326 IGIAGWVAOTKO-----MINIKEAYKDARENCEIDKLTGYTKTNAILCIPICNVEGDIIG 379
 QY 88 VQAQAINKIPGAPPTDEDDKVMOMYLPPFCGIAISNAQLFAASKEYERSALLLEVNDLFL 147
 Db 380 VQAIIINKTGCMFEFDEHDVEIFRRLYTFGIGIGIONAQLFEMSVOEQRRNOILLNARSIF 439
 QY 148 EQOTDLEKLVKKIMHRAOTLLKCCERCSVLLJE-----DIESP-----VVKFTK 190
 Db 440 EEONNLECLVTKIMTEARELLKCCERCSVFLVDLDOCCESASHLEKIIIEKPNOPATRAIKSAD 499
 QY 191 SEF-----LMSPKGSADAENSEFKESMEKSSYSWMLINNSIAELVASTGLPVNISD 240
 Db 500 SPEEKKMRNFTVLFFELGGYQAANVSRSVSELSSSTLA--QIAQVATTQTGVNICD 556
 QY 241 A-----YODPRDAEADQISGPHIRSVLCVPIWNSNHQIIGVAQVNLRLDGPFDQDQ 294
 Db 557 VIEWVRDHQIRAEDEIDS-----TQAILCMPIMNAQKKVIGVAQILINKANGVPFTDSDA 611
 QY 295 RLFEAFVIFCGIGINNTIMYDQVKKSWAKOSVALDVLSYHATCSKAEVDKFAANIPLVS 354
 Db 612 SIFEAFVIFCGIGIHTQMTENNACKLMKOKVALECLSYHATASQOOTEKLTODVTAEE 671
 QY 355 ELAIDDIHFDDSLDVDAMITAAALRMFMELGMVQKEIDYETLCRWLLTVYKKNYRMVLXH 414
 Db 672 SYNLYSFTTDFDELVDVDDTCRAVLRMFMOCNLVSQFIPYDVLCRVLSVRKNYRPVKYH 731
 QY 415 NWRHAFNVCOLMFAMLTITAGFQDILTEVEILAVIVGCLCHDLDRGTNNAFAKSSALA 474
 Db 732 NWRHALNVAQTMFAMLTGKMERFMTDLEILGLLVACLCHDLDRGTNNAFOTKTESPLA 791
 QY 475 QLYGTSATLEHHHFNH-----490
 Db 792 ILY-TTSTMEHHHFDHFLAAFLDLRAAFRRALRDLARELLDLVEELVVDPTLIFLVIEY 850
 QY 491 -----AVMILQS-----497
 Db 851 FRLRLRTILFPELDEEDDDVVDSVVVSVLVSVLVDSVLVLSAALTWATYKTIER 910
 QY 498 ----EGHNIFANLSKEYSDLMOLLKOSILATOLTYFFERTFEFFELVSGEYDWNINKH 553
 Db 911 TKTRDNFMDLSDPEDYRSVMKTVESAILSTDLAMYFKKNAPFLVELVNGEFDQGECK 970
 QY 554 RDIERSMLTACDLGAVTKPWEISROVAELVTSEFFEQDGRERLEKLTPSAIFDRNRKD 613
 Db 971 KDLLCGMMMTACDVSAIAKPWEVQHKVAKIVADEFFDQDGLKQLQNTQVAMMDREKRD 1030
 QY 614 ELPRLOLEWIDSICMPLYQALVKVNVKLPMLDSVATNRSKWEELHOK 661
 Db 1031 ELPMQGVGFDVLCILPLYRVLCDTFFWITPLYESTLENRRNWQDLAEK 1078

RESULT 13

AAV84879

ID AAY84879 standard; Protein; 1126 AA.

XX AAY84879;

XX 21-AUG-2000 (first entry)

DE Amino acid sequence of a PDE5D-GFP fusion protein.

XX I-kappaB kinase; cyclic nucleotide phosphodiesterase; cyclic AMP;
 KW cyclic GMP; PDE3; PDE7; PDE8; PDE4 splice variant; PDE4D;
 KW inflammatory disease; chronic inflammation; airway disease; asthma;
 KW chronic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis;
 KW pelvospodvilitis; bowel disease; ulcerative colitis; Crohn's disease;
 KW autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis;
 KW systemic lupus erythematosus; myasthenia gravis; Grave's disease;
 KW immune thrombocytopenic purpura; acute respiratory distress syndrome;
 KW septic shock; depression; PDE1; PDE2; PDE5; PDE9; PDE10; jet lag;

QY	221	---	INNSTAEVLVASTGLPVTNSDAYQDPQPRFDEADQISGFH---	IRSVLCVPIWN-SNHQ	2739
Db	404	ANKINMYAQVYKNTMEPLNIPDVSKKRFPWT	TENTGNVNOQCIRISLLCTPIKNGKKNK	463	
QY	274	IIGVAQVLNRLDG----	KPEDDADORLFEAFVIFCGLGINNTIMYDOVKKSWAKOSVAL	328	
Db	464	VIGVQOLYKMKBEENTGKVKPFNRNDEQ	FLFAFVIFCGLGTONTOMYEAVERAMAKOMVTL	5233	
QY	329	DVLSYHATCSK----	AEVDKFKAAANTPLVSELAIDD	IHFDDFSLDAMDITAALRMFMELG	3855
Db	524	EVLVSHASAAEETRELQSLAAAVVPSAOT	LKITDFFSEDFELSDLETALCTIRMTDLN	5833	
QY	386	MVQKFKIDYETLCRWLLTVRKNYRM-VLY	HNHRHAFNVCOLMFAMLTTFAGFODTLTEVEI	4444	
Db	584	LQVQFMKHEVLRCWILSVKKNYRKNVAY	HNHRHAFNTAOCMPAALKAGKIQNKLTDL	643	
QY	445	LAVIVGCLCHLDIRGTNNATQAKSGSALA	OLYCTSATLEHHHFNHAYMILQSEGHNIFA	5040	
Db	644	LALLAALSHLDHRGVNSYIQRSEHP	LAOLY-CHSIMEHHHFDQCLMLILNSPGNOILS	7022	
QY	505	NLSKSEYSDMLMOLLKOSLATLD	LYLPERRTFEFLVSKGEYDMWNIKNHRDIFRSLMLMTA	564	
Db	703	GLSIEEYKTTKIITKOA	ILDALYIKRGEFFELIRKNOFNLEDPHQKELFLAMILMTA	7623	
QY	565	CDLGAVTRPWEISRQVABELVTSEF	EQGDRERLELKTTPSAIFDRNRKDELPRQLQLEWID	624	
Db	763	CDLSAITKPWPIQRIAE	LVATEFEDQGDREKELNIEPTDLNREKKNKIPSMQVGFID	8222	
QY	625	SICMPLYALYKVVNVLKPM	LDVSATNRSKWEEL--HOKRLLASTASSS-----	6727	
Db	823	AICLOLYEALTHVSEDC	FFPLDGCGRKNRQKWALEOQEKMLINGESQAKRNVPRARD	8828	
QY	673	-PASVMVAK	680		
Db	883	PPVATMWSK	891		
RESULT 14					
AAV78940					
ID	AAV78940 standard; Protein: 832 AA.				
XX	AAV78940;				
XX	05-JUN-2000 (first entry)				
DE	Human phosphodiesterase V amino acid sequence #2:				
XX	Phosphodiesterase V; human; hypertension; pulmonary hypertension;				
KW	atherosclerosis, cerebral infarction; allergic rhinitis; kidney failure;				
KW	diabetic complication; glaucoma.				
XX	Homo sapiens.				
XX	WO200005383-AL.				
PN	03-FEB-2000.				
PD	19-JUL-1999; 99WO-JP03865.				
XX	21-JUL-1998; 98JP-0204964.				
PR	16-APR-1999; 99JP-0108974.				
XX	(TAKE) TAKEDA CHEM IND LTD.				
PA	Tarui N, Doi T, Nakahama K;				
XX	WPI: 2000-182705/16.				
DR	N-PSDB; AA295234.				
XX	New phosphodiesterase V useful for screening potential				
PT	phosphodiesterase inhibitors for treatment of hypertensive and allergic				
XX	diseases.				

Db 721 C D L S A I T K P W I Q O R I A E L V A T E F F D Q D R E R K E L N I E P T D L M N R E K K N I P S M Q V G F I D 780
QY 625 S I C M P L Y Q A L V K V N Y K L K P M L D S V A T N R S K W E E L - - H O K R L L A S T A S S S 672
Db 781 A I C L Q Y E A L T H V S E D C F P L D G C R K N R O K W Q A L A E Q O E K M L I N G E S G Q A 830

Search completed: June 13, 2003, 15:47:18
Job time : 62.4282 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:49:06 ; Search time 13.9203 Seconds
(without alignments)
1490.031 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975
Sequence: 1 MLKQARRPLFRNVLSTATQWK.....VLLIEDIESPVVFKTSFEL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	684	10	US-09-891-216-14
2	709	72.7	934	10	US-09-891-216-12
3	709	72.7	934	10	US-09-891-216-15
4	665.5	68.3	142	10	US-09-891-216-5
5	665.5	68.3	142	10	US-09-891-216-17
6	429	44.0	576	10	US-09-891-216-13
7	377	38.7	134	10	US-09-891-216-2
8	377	38.7	134	10	US-09-891-216-16
9	308.5	31.6	833	10	US-09-891-216-3
10	307.5	31.5	875	9	US-10-115-515-10
11	307.5	31.5	875	9	US-10-115-515-23
12	307.5	31.5	875	9	US-10-094-168B-5
13	186	19.1	367	9	US-10-094-168B-3
14	186	19.1	490	9	US-10-094-168B-1
15	165	16.9	779	10	US-09-420-190-1
16	165	16.9	789	10	US-09-321-801-2
17	165	16.9	791	10	US-09-321-801-4
18	165	16.9	796	10	US-09-321-801-15
19	162	16.6	905	12	US-10-094-989-4

20	162	16.6	920	12	US-10-094-989-2	Sequence 2, Appli
21	162	16.6	941	10	US-09-883-825-45	Sequence 45, Appl
22	160	16.4	300	10	US-09-321-801-13	Sequence 13, Appl
23	155.5	15.9	773	9	US-10-202-107-2	Sequence 2, Appli
24	154	15.8	921	10	US-09-883-825-39	Sequence 39, Appl
25	154	15.8	921	12	US-10-094-989-5	Sequence 5, Appli
26	154	15.8	942	10	US-09-883-825-43	Sequence 43, Appl
27	137	14.1	178	10	US-09-321-801-19	Sequence 19, Appl
28	92.5	9.5	1018	9	US-10-101-464A-909	Sequence 909, App
29	92	9.4	51	10	US-09-864-761-40569	Sequence 40569, A
30	80	8.2	499	10	US-09-883-080-2	Sequence 2, Appli
31	78.5	8.1	348	10	US-09-864-761-37615	Sequence 37615, A
32	78.5	8.1	439	9	US-09-056-019-37	Sequence 37, Appl
33	78	8.0	435	10	US-09-866-582-33	Sequence 33, Appl
34	78	8.0	600	10	US-09-975-901-2	Sequence 2, Appli
35	78	8.0	830	9	US-10-033-245-7	Sequence 7, Appli
36	78	8.0	830	9	US-10-033-223-7	Sequence 7, Appli
37	78	8.0	830	9	US-10-033-167-7	Sequence 7, Appli
38	78	8.0	830	9	US-10-033-244-7	Sequence 7, Appli
39	78	8.0	830	9	US-10-033-435-7	Sequence 7, Appli
40	78	8.0	830	9	US-10-032-990-7	Sequence 7, Appli
41	78	8.0	830	9	US-10-032-996-7	Sequence 7, Appli
42	78	8.0	830	9	US-10-033-396-7	Sequence 7, Appli
43	78	8.0	830	12	US-10-033-246-7	Sequence 7, Appli
44	78	8.0	830	12	US-10-033-301-7	Sequence 7, Appli
45	78	8.0	830	12	US-10-033-326-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-891-216-14
; Patent 14, Application US/09891216
; Sequence No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Phosphodiesterase-Like Enzyme
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-14

Query Match	100.0%	Score	975;	DB	10;	Length	684;
Best Local Similarity	100.0%	Pred. No.	1.2e-90;				
Matches	194;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MLKQARRPLFRNVLSTATQWKVITRLVQISGASLAEOEKHQDFLIQRTQTKDRRND	60				
Db	1	MLKQARRPLFRNVLSTATQWKVITRLVQISGASLAEOEKHQDFLIQRTQTKDRRND	60				
QY	61	EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMLPFCGIAI	120				
Db	61	EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDDEKVMQMLPFCGIAI	120				
QY	121	SNALFAASRKEVERSRALLEVVNDLFEETOLEKIVKKIMHRAOTLLKRCRCSVLLLED	180				
Db	121	SNALFAASRKEVERSRALLEVVNDLFEETOLEKIVKKIMHRAOTLLKRCRCSVLLLED	180				
QY	181	IESPVVFKTSFEL	194				

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Db      181 IESPVVKTKSFEL 194
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RESULT 2
US-09-891-216-12
; Sequence 12, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-12

Query Match      72.7%; Score 709; DB 10; Length 934;
Best Local Similarity 99.3%; Pred. No. 2.1e-63;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      54 KDRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYL 113
Db      304 QDRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYL 363
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Qy      114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
Db      364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
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Qy      174 SVLLEDIESPVVKTKSFEL 194
Db      424 SVLLEDIESPVVKTKSFEL 444
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RESULT 4
US-09-891-216-5
; Sequence 5, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-5

Query Match      68.3%; Score 665.5; DB 10; Length 142;
Best Local Similarity 95.0%; Pred. No. 4.2e-60;
Matches 133; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy      55 DRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYLP 114
Db      1 DRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYLP 60
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Qy      115 FCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 174
Db      61 FCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 120
|||||

Qy      175 VLLLEDIESPVVKTKSFEL 194
Db      121 VLLLEDIESPVVKTKSFEL 139
|||||

RESULT 5
US-09-891-216-17
; Sequence 17, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-15

Query Match      72.7%; Score 709; DB 10; Length 934;
Best Local Similarity 99.3%; Pred. No. 2.1e-63;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      54 KDRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYL 113
Db      304 QDRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYL 363
|||||

Qy      114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
Db      364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
|||||

Qy      174 SVLLEDIESPVVKTKSFEL 194
Db      424 SVLLEDIESPVVKTKSFEL 444
|||||

RESULT 3
US-09-891-216-15
; Sequence 15, Application US/09891216
; Patent No. US20020103120A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: Regulation of Human
; FILE REFERENCE: 02973.00511
; CURRENT APPLICATION NUMBER: US/09/891,216
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/213,998
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/293,221
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/EP01/07289
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 934
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-216-15

Query Match      72.7%; Score 709; DB 10; Length 934;
Best Local Similarity 99.3%; Pred. No. 2.1e-63;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      54 KDRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYL 113
Db      304 QDRRENDEIDKLTGYKTKSLLCMPITRSSDGEIIGVAAQAINKIPEGAPTEDEKVMQYL 363
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Qy      114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
Db      364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
|||||

Qy      174 SVLLEDIESPVVKTKSFEL 194
Db      424 SVLLEDIESPVVKTKSFEL 444
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; PRIOR FILING DATE: 2001-06-26
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 142
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-891-216-17

Query Match 68.3%; Score 665.5; DB 10; Length 142;
 Best Local Similarity 95.0%; Pred. No. 4.2e-60;
 Matches 133; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 55 DRFNDKLTGKTKSLCMLPSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMLP 114
 Db 1 DRFNDKLTGKTKSLCMLPSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMLP 60
 QY 115 FCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCRCS 174
 Db 61 FCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCRCS 120
 QY 175 VLLLEDIESPVVKTKSFEL 194
 Db 121 VLLLEDIESP-VSYLLSFKV 139

RESULT 6

US-09-891-216-13
 ; Sequence 13, Application US/09891216
 ; Patent No. US20020103120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Shyam
 ; TITLE OF INVENTION: Regulation of Human
 ; FILE REFERENCE: 02973.00511
 ; CURRENT APPLICATION NUMBER: US/09/891,216
 ; PRIOR FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: US 60/213,998
 ; PRIOR FILING DATE: 2000-06-26
 ; PRIOR APPLICATION NUMBER: US 60/293,221
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07289
 ; PRIOR FILING DATE: 2001-06-26
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 576
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-891-216-13

Query Match 44.0%; Score 429; DB 10; Length 576;
 Best Local Similarity 100.0%; Pred. No. 3.1e-35;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 109 MQMLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLL 168
 Db 1 MQMLPFCGIAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLL 60
 QY 169 KCERCSVLLLEDIESPVVKTKSFEL 194
 Db 61 KCERCSVLLLEDIESPVVKTKSFEL 86

RESULT 7

US-09-891-216-2
 ; Sequence 2, Application US/09891216
 ; Patent No. US20020103120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Shyam
 ; TITLE OF INVENTION: Regulation of Human
 ; FILE REFERENCE: 02973.00511

; CURRENT APPLICATION NUMBER: US/09/891,216
 ; CURRENT FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: US 60/213,998
 ; PRIOR FILING DATE: 2000-06-26
 ; PRIOR APPLICATION NUMBER: US 60/293,221
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07289
 ; PRIOR FILING DATE: 2001-06-26
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 134
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(134)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-891-216-2

Query Match 38.7%; Score 377; DB 10; Length 134;
 Best Local Similarity 68.9%; Pred. No. 8.3e-31;
 Matches 82; Conservative 3; Mismatches 4; Indels 30; Gaps 2;
 QY 105 DEKVMQMLPFCGIAISNAQLFAASRKEYERSR----- 137
 Db 3 DNKVMQMLPFCGIAISNAQLFAASRKEYERSRVDVLYKMSQVXPRTCFLLIVRKS 62
 QY 138 --ALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCRCSVLLLEDIESPVVKTKSFEL 194
 Db 63 CFALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCRCSVLLLEDIESP-VSYLLSFKV 120

RESULT 8

US-09-891-216-16
 ; Sequence 16, Application US/09891216
 ; Patent No. US20020103120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Shyam
 ; TITLE OF INVENTION: Regulation of Human
 ; FILE REFERENCE: 02973.00511
 ; CURRENT APPLICATION NUMBER: US/09/891,216
 ; CURRENT FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: US 60/213,998
 ; PRIOR FILING DATE: 2000-06-26
 ; PRIOR APPLICATION NUMBER: US 60/293,221
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07289
 ; PRIOR FILING DATE: 2001-06-26
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 134
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(134)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-891-216-16

Query Match 38.7%; Score 377; DB 10; Length 134;
 Best Local Similarity 68.9%; Pred. No. 8.3e-31;
 Matches 82; Conservative 3; Mismatches 4; Indels 30; Gaps 2;
 QY 105 DEKVMQMLPFCGIAISNAQLFAASRKEYERSR----- 137
 Db 3 DNKVMQMLPFCGIAISNAQLFAASRKEYERSRVDVLYKMSQVXPRTCFLLIVRKS 62
 QY 138 --ALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCRCSVLLLEDIESPVVKTKSFEL 194
 Db 63 CFALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCRCSVLLLEDIESP-VSYLLSFKV 120

	APPLICATION NUMBER: US/10/115,515	
	FILING DATE: 03-Apr-2002	
	CLASSIFICATION: <Unknown>	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US/09/599,658	
	FILING DATE: 21-Jun-2000	
	APPLICATION NUMBER: 09/055,584	
	FILING DATE: 4-JUNE-1998	
	ATTORNEY/AGENT INFORMATION:	
	NAME: NO. US20030054992Aland, Greta E.	
	REGISTRATION NUMBER: 35,302	
	REFERENCE/DOCKET NUMBER: 32706	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (312) 474-6300	
	TELEFAX: (312) 474-0448	
	TELEX: 25-3856	
	INFORMATION FOR SEQ ID NO: 23:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 875 amino acids	
	TYPE: amino acid	
	TOPOLOGY: linear	
	MOLECULE TYPE: protein	
	SEQUENCE DESCRIPTION: SEQ ID NO: 23:	
US-10-115-515-23		
Query Match	31.5%; Score 307.5; DB 9; Length 875;	
Best Local Similarity	46.1%; Pred. No. 1.2e-22;	
Matches	59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;	
Qy	54 KDRFNDEIDKLTGYKTKSLCMLPRTSSDGEIIGVAAQAIN-KIEGAPFTEDDEKVQMOMY 112	
Db	247 EDPRFAEVDQITGYKTQSILCMPIKNHRREVGVAAQINKKSGNGTFTTEKDKDFAAY 306	
Qy	113 LPFCGLAISNAQLFAASRKEYERSRALLEVNDLFEQOTOLEKIVKKIMHRAQTLLKCR 172	
Db	307 LAFCGVLHNAQLYETLSLENKRNVLLDLASLIFEQQSLEVLIIKTAATIISFMQVOK 366	
Qy	173 CSVLLED 180	
Db	367 CTIFIVDE 374	
RESULT 12		
US-10-094-168B-5		
Sequence 5, Application US/10094168B		
Publication No. US20030092156A1		
GENERAL INFORMATION:		
APPLICANT: Phillips, Stephen C.; Harrow, Ian		
APPLICANT: Lanfear, Jerry; Fawcett, Lindsay		
APPLICANT: Bandman, Olga		
TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES		
FILE REFERENCE: PF-0623-2 CIP		
CURRENT APPLICATION NUMBER: US/10/094,168B		
CURRENT FILING DATE: 2002-11-13		
PRIOR APPLICATION NUMBER: US 09/595,514		
PRIOR FILING DATE: 2000-06-14		
PRIOR APPLICATION NUMBER: US 09/226,741		
PRIOR FILING DATE: 1999-01-07		
NUMBER OF SEQ ID NOS: 7		
SOFTWARE: PERL Program		
SEQ ID NO 5		
LENGTH: 875		
TYPE: PRT		
ORGANISM: Homo sapiens		
FEATURE:		
NAME/KEY: misc_feature		
OTHER INFORMATION: GenBank ID No. US20030092156A1 g3355606		
US-10-094-168B-5		
Query Match	31.5%; Score 307.5; DB 9; Length 875;	
Best Local Similarity	46.1%; Pred. No. 1.2e-22;	
Matches	59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;	

Qy	54 KDRFNDEIDKLTGYKTKSLCMLPRTSSDGEIIGVAAQAIN-KIEGAPFTEDDEKVQMOMY 111	
Db	247 EDPRFAEVDQITGYKTQSILCMPIKNHRREVGVAAQINKKSGNGTFTTEKDKDFAAY 306	
Qy	113 LPFCGLAISNAQLFAASRKEYERSRALLEVNDLFEQOTOLEKIVKKIMHRAQTLLKCR 172	
Db	307 LAFCGVLHNAQLYETLSLENKRNVLLDLASLIFEQQSLEVLIIKTAATIISFMQVOK 366	
Qy	173 CSVLLED 180	
Db	367 CTIFIVDE 374	
RESULT 13		
US-10-094-168B-3		
Sequence 3, Application US/10094168B		
Publication No. US20030092156A1		
GENERAL INFORMATION:		
APPLICANT: Phillips, Stephen C.; Harrow, Ian		
APPLICANT: Lanfear, Jerry; Fawcett, Lindsay		
APPLICANT: Bandman, Olga		
TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES		
FILE REFERENCE: PF-0623-2 CIP		
CURRENT APPLICATION NUMBER: US/10/094,168B		
CURRENT FILING DATE: 2002-11-13		
PRIOR APPLICATION NUMBER: US 09/595,514		
PRIOR FILING DATE: 2000-06-14		
PRIOR APPLICATION NUMBER: US 09/226,741		
PRIOR FILING DATE: 1999-01-07		
NUMBER OF SEQ ID NOS: 7		
SOFTWARE: PERL Program		
SEQ ID NO 3		
LENGTH: 367		
TYPE: PRT		
ORGANISM: Homo sapiens		
FEATURE:		
NAME/KEY: misc_feature		
OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A2		
US-10-094-168B-3		
Query Match	19.1%; Score 186; DB 9; Length 367;	
Best Local Similarity	29.7%; Pred. No. 8.4e-11;	
Matches	38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;	
Qy	34 SLAEKQEK--HODFLIORQTKT-----KDRRNDEIDKLTGYKTKSLCMLCM 76	
Db	12 SFKSEMEKSSYDWLNNSIAELVASTGLPVNSIDAYQDPFRDAEQDSGFHRSVLCV 71	
Qy	77 PIRSDGEIIGVAAQAINKIPEGAFTEDDEKVQMOMLPFGCAISNAQLFAASRKEYERS 136	
Db	72 PINWNNHIIGVAAQVNLRL-DGKPFDDADQRLFEAFVFCGLGINNTIMYDVVKKSQAQ 130	
Qy	137 RALLEVVN 144	
Db	131 SVALDVLS 138	
RESULT 14		
US-10-094-168B-1		
Sequence 1, Application US/10094168B		
Publication No. US20030092156A1		
GENERAL INFORMATION:		
APPLICANT: Phillips, Stephen C.; Harrow, Ian		
APPLICANT: Lanfear, Jerry; Fawcett, Lindsay		
APPLICANT: Bandman, Olga		
TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES		
FILE REFERENCE: PF-0623-2 CIP		
CURRENT APPLICATION NUMBER: US/10/094,168B		
CURRENT FILING DATE: 2002-11-13		
PRIOR APPLICATION NUMBER: US 09/595,514		
PRIOR FILING DATE: 2000-06-14		
PRIOR APPLICATION NUMBER: US 09/226,741		
PRIOR FILING DATE: 1999-01-07		
NUMBER OF SEQ ID NOS: 7		
SOFTWARE: PERL Program		
SEQ ID NO 5		
LENGTH: 875		
TYPE: PRT		
ORGANISM: Homo sapiens		
FEATURE:		

Qy	54	KDRFNDEIDKLTGYKTKSLCMLP	IRSSDGEIIGVAAQAIN-KIPEGAPFTEDEKVMQMY 111
Db	247	EDPRFNAEVDQITGYKTSILCMP	IKNHREVVGVAAQINKKSGNGTFTTEKDEKFAAY 306
Qy	113	LPFCGLAISNAQLFAASRKEYERS	RALLLEVNDLFEQOTOLEKIVKIMHRAOTLLKCR 172
Db	307	LAFCGVLHNAQLYETSLLENKRNQ	VLLDLASLIFEQQSLEVLKIAATIIISFMQVOK 366
Qy	173	CSVLLED 180	
Db	367	CTIFIVDE 374	
<p>RESULT 13</p> <p>US-10-094-168B-3</p> <p>Sequence 3, Application US/10094168B</p> <p>Publication No. US20030092156A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Phillips, Stephen C.; Harrow, Ian</p> <p>APPLICANT: Lanfear, Jerry; Fawcett, Lindsay</p> <p>APPLICANT: Bandman, Olga</p> <p>TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES</p> <p>FILE REFERENCE: PF-0623-2 CIP</p> <p>CURRENT APPLICATION NUMBER: US/10/094,168B</p> <p>CURRENT FILING DATE: 2002-11-13</p> <p>PRIOR APPLICATION NUMBER: US 09/595,514</p> <p>PRIOR FILING DATE: 2000-06-14</p> <p>PRIOR APPLICATION NUMBER: US 09/226,741</p> <p>PRIOR FILING DATE: 1999-01-07</p> <p>NUMBER OF SEQ ID NOS: 7</p> <p>SOFTWARE: PERL Program</p> <p>SEQ ID NO 3</p> <p>LENGTH: 367</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>NAME/KEY: misc_feature</p> <p>OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A2</p> <p>US-10-094-168B-3</p>			
<p>Query Match 19.1%; Score 186; DB 9; Length 367;</p> <p>Best Local Similarity 29.7%; Pred. No. 8.4e-11;</p> <p>Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;</p>			
Qy	34	SLAEKQEK--HODFLIORQTKT	-----KDRFNDEIDKLTGYKTKSLCML 76
Db	12	SFKESMEKSSYDWLNNSTAEVL	SVASTGLPYNISDAQDPRFPAEADQISGFHRSVLCV 71
Qy	77	PIRSSDGEIIGVAAQAINKIPEGA	PFTTEDEKVMQMYLPFCGLAISNAQLFAASRKEYERS 136
Db	72	PIWNSHIIIGVAAQVNLRL-DGK	PFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAQ 130
Qy	137	RALLEVN 144	
Db	131	SVALDVLS 138	
<p>RESULT 14</p> <p>US-10-094-168B-1</p> <p>Sequence 1, Application US/10094168B</p> <p>Publication No. US20030092156A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Phillips, Stephen C.; Harrow, Ian</p> <p>APPLICANT: Lanfear, Jerry; Fawcett, Lindsay</p> <p>APPLICANT: Bandman, Olga</p> <p>TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES</p> <p>FILE REFERENCE: PF-0623-2 CIP</p> <p>CURRENT APPLICATION NUMBER: US/10/094,168B</p> <p>CURRENT FILING DATE: 2002-11-13</p> <p>PRIOR APPLICATION NUMBER: US 09/595,514</p> <p>PRIOR FILING DATE: 2000-06-14</p> <p>PRIOR APPLICATION NUMBER: US 09/226,741</p> <p>PRIOR FILING DATE: 1999-01-07</p>			
<p>Query Match 31.5%; Score 307.5; DB 9; Length 875;</p> <p>Best Local Similarity 46.1%; Pred. No. 1.2e-22;</p> <p>Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;</p>			
Qy	54	KDRFNDEIDKLTGYKTKSLCMLP	IRSSDGEIIGVAAQAIN-KIPEGAPFTEDEKVMQMY 112
Db	247	EDPRFNAEVDQITGYKTSILCMP	IKNHREVVGVAAQINKKSGNGTFTTEKDEKFAAY 306
Qy	113	LPFCGLAISNAQLFAASRKEYERS	RALLLEVNDLFEQOTOLEKIVKIMHRAOTLLKCR 172
Db	307	LAFCGVLHNAQLYETSLLENKRNQ	VLLDLASLIFEQQSLEVLKIAATIIISFMQVOK 366
Qy	173	CSVLLED 180	
Db	367	CTIFIVDE 374	
<p>RESULT 12</p> <p>US-10-094-168B-5</p> <p>Sequence 5, Application US/10094168B</p> <p>Publication No. US20030092156A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Phillips, Stephen C.; Harrow, Ian</p> <p>APPLICANT: Lanfear, Jerry; Fawcett, Lindsay</p> <p>APPLICANT: Bandman, Olga</p> <p>TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING CYCLIC NUCLEOTIDE PDES</p> <p>FILE REFERENCE: PF-0623-2 CIP</p> <p>CURRENT APPLICATION NUMBER: US/10/094,168B</p> <p>CURRENT FILING DATE: 2002-11-13</p> <p>PRIOR APPLICATION NUMBER: US 09/595,514</p> <p>PRIOR FILING DATE: 2000-06-14</p> <p>PRIOR APPLICATION NUMBER: US 09/226,741</p> <p>PRIOR FILING DATE: 1999-01-07</p> <p>NUMBER OF SEQ ID NOS: 7</p> <p>SOFTWARE: PERL Program</p> <p>SEQ ID NO 5</p> <p>LENGTH: 875</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>NAME/KEY: misc_feature</p> <p>OTHER INFORMATION: GenBank ID No. US20030092156A1 g3355606</p> <p>US-10-094-168B-5</p>			
<p>Query Match 31.5%; Score 307.5; DB 9; Length 875;</p> <p>Best Local Similarity 46.1%; Pred. No. 1.2e-22;</p> <p>Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;</p>			

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030092156A1 HSPDE10A1
US-10-094-168B-1

Query Match 19.1%; Score 186; DB 9; Length 490;
Best Local Similarity 29.7%; Pred. No. 1.2e-10;
Matches 38; Conservative 35; Mismatches 37; Indels 18; Gaps 3;
QY 34 SLAEKQEK--HQDFLIQRTKT-----KDRFNDKIDKLTGKTKSLLCM 76
Db 12 SFKSMKSSYSDDLNNISIAELVASTGLPVNISDAYODPRDAEQISGFHRSVLCV 71
QY 77 PIRSDGRIIGVAQAINKIPGAPFTEDEKVMQMYLPFCGIAISNAOLFASRKEYERS 136
Db 72 PIWNSNHOIIGVAQVNLNL-DGKPFDDADQRLFEAFVIFCGLGINNNTIMYDQVKSWAKQ 130
QY 137 RALLEVN 144
Db 131 SVALDVLS 138

RESULT 15
US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-420-190-1

Query Match 16.9%; Score 165; DB 10; Length 779;
Best Local Similarity 45.8%; Pred. No. 3.2e-08;
Matches 33; Conservative 15; Mismatches 22; Indels 2; Gaps 2;
QY 55 DRRFNDEIDKLTGKTKSLLCMPIRSSDGEIIGVAQAINKIPGAPFTEDEKVMQMYLP 114
Db 349 DPRENREVDLYTGYTRNLCMPI-VSRGSVIGVQMVNKI-SGSAFSKTDENNFKMFAV 406
QY 115 FCGIAISNAQLF 126
Db 407 FCALALHCANNY 418

Search completed: June 13, 2003, 15:59:22
Job time : 14.9203 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:38:09 ; Search time 16.5718 Seconds
(without alignments)
1559.921 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNVLNLSATQWK.....VLLIEDIESPVVKFTKSFEL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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4: /SID22/qcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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21: /SID22/qcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/qcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/qcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	684	22	Human type 11 phos
2	975	100.0	684	22	Human cyclic nucle
3	882	90.5	685	22	Rat type 11 phosph
4	709	72.7	934	22	Human type 11 phos
5	705	72.3	935	22	Rat type 11 phosph
6	665.5	68.3	142	23	Human phosphodiester
7	429	44.0	576	22	Amino acid sequenc
8	376.5	38.6	135	23	Human phosphodiester
9	354.5	36.4	1232	22	Drosophila melanog
10	349	35.8	1284	22	Drosophila melanog

11	349	35.8	1284	23	ABB08376	D. melanogaster CG
12	307.5	31.5	494	19	AAW42013	cGMP-binding phosph
13	307.5	31.5	549	19	AAW42014	cGMP-binding phosph
14	307.5	31.5	832	21	AAW78939	Human phosphodiester
15	307.5	31.5	832	21	AAW78940	Human phosphodiester
16	307.5	31.5	833	21	AAW90912	Human cGMP phospho
17	307.5	31.5	833	22	AAW97024	Human phosphodiester
18	307.5	31.5	875	16	AAW66565	Cyclic guanosine m
19	307.5	31.5	875	19	AAW42011	Bovine cGMP-binding
20	307.5	31.5	875	20	AAW14990	Bovine cGMP-binding
21	307.5	31.5	875	20	AAW14991	Human cGMP-binding
22	307.5	31.5	1126	21	AAW84879	Amino acid sequenc
23	301.5	30.9	875	16	AAW66564	Cyclic guanosine m
24	203	20.8	930	23	AAU79716	Trypanosoma brucei
25	199	20.4	930	23	AAU79718	Trypanosoma brucei
26	186	19.1	367	21	AAW95522	Human cyclic nucle
27	186	19.1	490	21	AAW95521	Human cyclic nucle
28	182.5	18.7	474	22	AAW67531	Amino acid sequenc
29	165	16.9	135	21	AAW53949	Peptide representi
30	165	16.9	749	21	AAW53959	Formula III repres
31	165	16.9	750	21	AAW53960	Formula IV repres
32	165	16.9	754	21	AAW53961	Formula V repres
33	165	16.9	758	21	AAW53962	Formula VI repres
34	165	16.9	759	21	AAW53972	Amino acid sequenc
35	165	16.9	766	20	AAW13934	Human phosphodiester
36	165	16.9	766	22	AAW28256	Human phosphodiester
37	165	16.9	767	21	AAW53963	Formula VII repres
38	165	16.9	774	21	AAW57306	Rat phosphodiester
39	165	16.9	779	20	AAW13936	Human phosphodiester
40	165	16.9	779	21	AAW26853	Human phosphodiester
41	165	16.9	779	22	AAW73486	Human cyclic nucle
42	165	16.9	779	22	AAW28258	Human phosphodiester
43	165	16.9	788	21	AAW26856	Human phosphodiester
44	165	16.9	789	21	AAW26854	Human phosphodiester
45	165	16.9	789	21	AAW53935	A human phosphodie

ALIGNMENTS

RESULT 1
AAG62678
ID AAG62678 standard; Protein; 684 AA.
AC AAG62678;
XX
XX
DT 19-SEP-2001 (first entry)
DE Human type 11 phosphodiesterase SEQ ID NO: 4.
DE Human type 11 phosphodiesterase; PDE11; signal transduction;
KW Human; type 11 phosphodiesterase; selective inhibition.
KW selective inhibition.
XX
XX Homo sapiens.
OS
XX
XX WO200146436-A1.
PN
XX
PD 28-JUN-2001.
PD
XX
XX 22-DEC-2000; 2000WO-JP09118.
PF
XX
XX 22-DEC-1999; 99JP-0364866.
PR
XX
XX 01-JUN-2000; 2000JP-0163875.
PR
XX
XX (TANA) TANABE SEIYAKU CO.
PA
XX
XX Omori K, Yuasa K, Kotera J, Oda K, Michibata H;
PI
XX
XX WPI: 2001-418074/44.
DR
XX
XX N-PSDB; AAH46709.
PT
XX
XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular

PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy

PS Claim 2; Page 49-51; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX Sequence 684 AA;

Query Match 100.0%; Score 975; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 5.5e-96;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRFND 60
Db 1 MLQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRFND 60
Qy 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120
Db 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120
Qy 121 SNAOLFASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180
Db 121 SNAOLFASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180
Qy 181 IESPVKFTKSFEL 194
Db 181 IESPVKFTKSFEL 194

RESULT 2

AAB35472
ID AAB35472 standard; protein: 684 AA.

XX AC AAB35472;

XX DT 06-JUN-2001 (first entry)

XX DE Human cyclic nucleotide phosphodiesterase PDEXV.

XX KW Human; cyclic nucleotide phosphodiesterase; PDEXV; sexual dysfunction;
KW cardiovascular disease; gastrointestinal disorder; corpus cavernosum;
KW kidney; liver; skeletal muscle; testis prostate; spleen.

XX OS Homo sapiens.

XX PN EP1085089-A2.

XX PD 21-MAR-2001.

XX PF 14-SEP-2000; 2000EP-0307981.

XX PR 17-SEP-1999; 99GB-0022124.

XX PA (PFIZ) PFIZER LTD.

XX PA (PFIZ) PFIZER INC.

XX PI Fidock MD, Robas NM;

XX WPI; 2001-246900/26.

XX DR N-PSDB; AAF62311.

XX Human cyclic nucleotide phosphodiesterase and its nucleotide sequence
PT useful for treating cardiovascular disorders, sexual dysfunction and
PT screening for drugs to treat associated disorders

PS Claim 1; Page 37-41; 44pp; English.

XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX

Sequence 684 AA;

Query Match 100.0%; Score 975; DB 22; Length 684;
Best Local Similarity 100.0%; Pred. No. 5.5e-96;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRFND 60
Db 1 MLQARRPLFRNVL SATQWKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRFND 60
Qy 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120
Db 61 EIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGIAI 120
Qy 121 SNAOLFASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180
Db 121 SNAOLFASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLLKCERC SVLLLED 180
Qy 181 IESPVKFTKSFEL 194
Db 181 IESPVKFTKSFEL 194

RESULT 3

AAG62679
ID AAG62679 standard; Protein: 685 AA.

XX AC AAG62679;

XX DT 19-SEP-2001 (first entry)

XX DE Rat type 11 phosphodiesterase SEQ ID NO: 6.

XX KW Rat; type 11 phosphodiesterase; PDE11; signal transduction;
KW selective inhibition.

XX OS Rattus sp.

XX PN WO200146436-A1.

XX PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-JP09118.

XX PR 22-DEC-1999; 99JP-0364866.

XX PR 01-JUN-2000; 2000JP-0163875.

XX PA (TANA) TANABE SEIYAKU CO.

XX PI Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX WPI; 2001-418074/44.

XX DR N-PSDB; AAH46710.

XX Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy

XX Claim 2; Page 55-57; 77pp; Japanese.

XX The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for

CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX Sequence 685 AA;

Query Match 90.5%; Score 882; DB 22; Length 685;
Best Local Similarity 90.7%; Pred. No. 5.7e-86;
Matches 176; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MLKARRPLFNVL SATQKKVKITRLVQISGASLAEKQKHQDFLQRTKTKDRRND 60
DB 1 MLKARRFNFVRVSATQRRKVGSTROGQISGAFLAERLDKHQDFLTMQTRTKDRRND 60
QY 61 EIDKLTGYKTKSLLCMPTRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGTAI 120
DB 61 EIDKLTGYKTKSLLCMPTRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYLPFCGTAI 120
QY 121 SNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC SVLLLED 180
DB 121 SNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC SVLLLED 180
QY 181 IESPVVKETKSFEL 194
DB 181 IESPVVKETKSFEL 194

RESULT 4

AAG62677
ID AAG62677 standard; Protein; 934 AA.

XX AC AAG62677;

XX DT 19-SEP-2001 (first entry)

XX DE Human type 11 phosphodiesterase SEQ ID NO: 2.

XX KE Human; type 11 phosphodiesterase; PDE11; signal transduction;
XX KW selective inhibition.

XX OS Homo sapiens.

XX PN WO200146436-A1.

XX PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-JP09118.

XX PR 22-DEC-1999; 99JP-0364866.

XX PR 01-JUN-2000; 2000JP-0163875.

XX PA (TANA) TANABE SEIYAKU CO.

XX PI Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX DR WPI; 2001-418074/44.

XX DR N-PSDB; AAH46708.

XX PT Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy .

XX PS Claim 2; Page 42-45; 77pp; Japanese.

XX CC The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms. In screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present

CC sequence is a protein of the invention.

XX SQ Sequence 934 AA;

Query Match 72.7%; Score 709; DB 22; Length 934;
Best Local Similarity 99.3%; Pred. No. 3.7e-67;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 54 KDRFNDEIDKLTGYKTKSLLCMPTRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYL 113
DB 304 QDRFNDEIDKLTGYKTKSLLCMPTRSSDGEIIGVAQAINKIPEGAPTEDEKVMQMYL 363
QY 114 PFCGTAINAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 173
DB 364 PFCGTAINAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423
QY 174 SVLLLEDIESPVVKETKSFEL 194
DB 424 SVLLLEDIESPVVKETKSFEL 444

RESULT 5

AAG62680

ID AAG62680 standard; Protein; 935 AA.

XX AC AAG62680;

XX DT 19-SEP-2001 (first entry)

XX DE Rat type 11 phosphodiesterase SEQ ID NO: 39.

XX KE Rat; type 11 phosphodiesterase; PDE11; signal transduction;
XX KW selective inhibition.

XX OS Rattus sp.

XX PN WO200146436-A1.

XX PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-JP09118.

XX PR 22-DEC-1999; 99JP-0364866.

XX PR 01-JUN-2000; 2000JP-0163875.

XX PA (TANA) TANABE SEIYAKU CO.

XX PI Omori K, Yuasa K, Kotera J, Oda K, Michibata H;

XX DR WPI; 2001-418074/44.

XX DR N-PSDB; AAH46742.

XX PT Type 11 phosphodiesterases and encoded genes with activity of
PT hydrolyzing cyclic nucleotides, useful for studying intracellular
PT signal transduction mechanism and in screening highly-selective
PT inhibitors as drugs with superior efficacy .

XX PS Claim 2; Page 69-72; 77pp; Japanese.

XX CC The present invention provides the protein and coding sequences of novel
CC human and rat type 11 phosphodiesterases (PDE11). These are useful for
CC studying intracellular signal transduction mechanisms, in screening
CC highly-selective inhibitors as drugs for treating diseases associated
CC with the enzymes and for the identification or selection of selective
CC inhibitory action against multiple type phosphodiesterases. The present
CC sequence is a protein of the invention.

XX SQ Sequence 935 AA;

Query Match 72.3%; Score 705; DB 22; Length 935;
Best Local Similarity 97.9%; Pred. No. 9.9e-67;
Matches 138; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY 54 KDRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQYL 113
Db 304 QDRFNDEIDKLTGYKTKSLLCMPIRNSDGEIIGVAQAINKVPEGAPTEDEKVMQYL 363
QY 114 PFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAOTLLKCERC 173
Db 364 PFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAOTLLKCERC 423
QY 174 SVLLEDIESPVVFKTSFEL 194
Db 424 SVLLEDIESPVVFKTSFEL 444

RESULT 6
AAE17789
ID AAE17789 standard; Protein; 142 AA.
XX
AC AAE17789;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human phosphodiesterase (PDE)-like enzyme #2.
XX
KW Human; phosphodiesterase; PDE-like enzyme; benign prostate hyperplasia;
KW urinary incontinence; erectile dysfunction; cardiovascular disorder;
KW cancer; diabetes; ischaemic disease; myocardial infarction; cytostatic;
KW vasodilator; cardiant.
XX
OS Homo sapiens.
XX
PN WO200200854-A2.
XX
PD 03-JAN-2002.
XX
PE 26-JUN-2001; 2001WO-EP07289.
XX
PR 26-JUN-2000; 2000US-213998P.
PR 25-MAY-2001; 2001US-293221P.
XX
PA (FARB ) BAYER AG.
XX
PI Ramakrishnan S;
XX
DR WPI; 2002-090522/12.
DR N-PSDB; AAD28571.
XX
PT Isolated polynucleotide encoding a human phosphodiesterase-like enzyme,
PT useful for treating a disease such as urinary incontinence, benign
PT prostate hyperplasia, erectile dysfunction, diabetes, cancer or
PT cardiovascular disorder.
XX
PS Claim 25; Fig 5; 165pp; English.
XX
CC The present invention relates to human phosphodiesterase (PDE)-like
CC enzymes and their corresponding polynucleotides. The invention also
CC relates to reagents which regulate PDE-like enzyme activity and reagents
CC which bind to human PDE-like enzyme gene products which can be used to
CC regulate degradation of cGMP. Sequences of the invention are useful for
CC modulating the activity of a PDE-like enzyme in a disease such as urinary
CC incontinence, benign prostate hyperplasia, erectile dysfunction, cancer,
CC diabetes or cardiovascular disorder (e.g. ischaemic diseases, myocardial
CC infarction). The present sequence is human PDE-like enzyme.
XX
SQ Sequence 142 AA;
Query Match 68.3%; Score 665.5; DB 23; Length 142;
Best Local Similarity 95.0%; Pred. No. 1.3e-63;
Matches 133; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 55 DRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQYLP 114
Db 1 DRFNDEIDKLTGYKTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPTEDEKVMQYLP 60
```

```
QY 115 FCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAOTLLKCERC 174
Db 61 FCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAOTLLKCERC 120
QY 175 VLLLEDIESPVVFKTSFEL 194
Db 121 VLLLEDIESP-VSYLLSEKV 139

RESULT 7
AAG67533
ID AAG67533 standard; Protein; 576 AA.
XX
AC AAG67533;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of a human phosphodiesterase polypeptide.
XX
KW Human; phosphodiesterase; diabetes; ischemic heart disease; hypertension;
KW nephritis; pancreatitis; ulcer; allergy; asthma; rheumatism;
KW osteoporosis; pain; anxiety; schizophrenia; manic depressive psychosis;
KW Parkinson's disease; dementia; infectious disease; malignant tumour.
XX
OS Homo sapiens.
XX
PN WO200166716-A1.
XX
PD 13-SEP-2001.
XX
PE 06-MAR-2001; 2001WO-JP01720.
XX
PR 07-MAR-2000; 2000JP-0061464.
PR 10-JUL-2000; 2000JP-0208610.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Miyaji H, Haruoka M, Ota T, Kawabata A, Sugano S, Nakamura Y;
XX
DR WPI; 2001-570769/64.
DR N-PSDB; AAH78232.
XX
PT Polypeptides with phosphodiesterase activity and DNA for treatment of
PT diabetes, ischemic heart disease, hypertension, nephritis,
PT pancreatitis, ulcers, allergies, asthma
XX
PS Claim 1; Page 90-93; 105pp; Japanese.
XX
CC The present sequence encodes a human polypeptide which has
CC phosphodiesterase activity. The phosphodiesterase polypeptide and
CC polynucleotide are used for the treatment and prevention of diabetes,
CC ischemic heart disease, hypertension, nephritis, pancreatitis, ulcers,
CC allergies, asthma, rheumatism, osteoporosis, pain, anxiety,
CC schizophrenia, manic depressive psychosis, Parkinson's disease,
CC dementia, infectious diseases, and malignant tumours.
XX
SQ Sequence 576 AA;
Query Match 44.0%; Score 429; DB 22; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.7e-37;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 MQMYPFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAOTLL 168
Db 1 MQMYPFCGTAISNAQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAOTLL 60
QY 169 KCERCSVLLLEDIESPVVFKTSFEL 194
Db 61 KCERCSVLLLEDIESPVVFKTSFEL 86

RESULT 8
AAE17789
```


1

123 AQLFAASRKEYERSRALLEVVNDLFEEQTDLEKIVKIMHRAQTLKERCVCVLLLEDIE 182

Db 382 AQLYKSOLEIKRNOVLDDLARMIFEEQSTIEHMFVFRILTHMQSLIOQVRQVILLVHEAD 441
Qy 183 SPVVKFTKSFE 193
Db 442 KG--SFSRVFD 450

RESULT 12
AAW42013
ID AAW42013 standard; protein; 494 AA.

AC AAW42013;

XX 28-MAY-1998 (first entry)

DE CGMP-binding phosphodiesterase fragment 2.

XX Human cGMP-binding phosphodiesterase: cGB-PDE; control sequence;
KW antibody.

XX Homo sapiens.

PN US5702936-A.

XX 30-DEC-1997.

PF 27-MAY-1994; 94US-0250847.

PR 27-MAY-1994; 94US-0250847.

PR 27-MAY-1993; 93US-0068051.

XX (ICOS-) ICOS CORP.

PA (UYVA-) UNIV VANDERBILT.

PA (UNIW) UNIV WASHINGTON.

XX Beavo JA, Corbin JD, Ferguson KM, Francis SH, Kadlecsek A;

PI Loughney K, McAllister-Lucas LM, Sonnenburg WK, Thomas MK;

XX WPI; 1998-076421/07.

PT Fragments of human cGMP-binding phosphodiesterase - used for
isolating modulators of cGB-PDE associated diseases

PS Claim 2; Pages -: 42pp; English.

XX This sequence is a fragment of the human cGMP-binding phosphodiesterase
(cGB-PDE), consisting of amino acid residues 1-494. The novel
polypeptide can be used for the detection of cGB-PDE and the isolation
of its expression control sequences. It can also be used to identify
genetic alterations in the cGB-PDE locus associated with diseases.
CC Antibodies specific for cGB-PDE fragments can also be used in detecting
CC and quantifying the amount of cGB-PDE present in samples.
CC (Note: this sequence is not given in the specification but is generated
CC from the defined wild type sequence).

XX Sequence 494 AA;

Query Match 31.5%; Score 307.5; DB 19; Length 494;
Best Local Similarity 46.1%; Pred. No. 2.6e-24;

Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;

Qy 54 KDRFNDEIDKLTGYKTKSLCMTPIRSSDGEIIGVQAQAIN-KIPEGAPFTEDEKVMQY 112
Db 247 EDPRENAEVDQITGYKTSILCMTPIKHNREEVGVQAQAINKSGNGTFTTEKDEKDFRAY 306

Qy 113 LPFGCIATSNALQFAASRKEYERSRALLEVVDLFEQOTDLEKIVKIMHRAQTLLKCR 172
Db 307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOQSLEVLILKTAATIIISFMQVQK 366

Qy 173 CSQLLED 180

Db 367 CTIFIVDE 374

RESULT 14
AAW78939

RESULT 13

AAW42014

XX AAW42014 standard; protein; 549 AA.

AC AAW42014;

XX 28-MAY-1998 (first entry)

DE CGMP-binding phosphodiesterase fragment 3.

XX Human cGMP-binding phosphodiesterase; cGB-PDE; control sequence;
KW antibody.

XX Homo sapiens.

PH Key Location/Qualifiers

PN US5702936-A.

XX 30-DEC-1997.

PF 27-MAY-1994; 94US-0250847.

PR 27-MAY-1994; 94US-0250847.

PR 27-MAY-1993; 93US-0068051.

XX (ICOS-) ICOS CORP.

PA (UYVA-) UNIV VANDERBILT.

PA (UNIW) UNIV WASHINGTON.

XX Beavo JA, Corbin JD, Ferguson KM, Francis SH, Kadlecsek A;

PI Loughney K, McAllister-Lucas LM, Sonnenburg WK, Thomas MK;

XX WPI; 1998-076421/07.

PT Fragments of human cGMP-binding phosphodiesterase - used for
isolating modulators of cGB-PDE associated diseases

PS Claim 3; Pages -: 42pp; English.

XX This sequence is a fragment of the human cGMP-binding phosphodiesterase
(cGB-PDE), consisting of amino acid residues 1-549. The novel
polypeptide can be used for the detection of cGB-PDE and the isolation
of its expression control sequences. It can also be used to identify
genetic alterations in the cGB-PDE locus associated with diseases.
CC Antibodies specific for cGB-PDE fragments can also be used in detecting
CC and quantifying the amount of cGB-PDE present in samples.
CC (Note: this sequence is not given in the specification but is generated
CC from the defined wild type sequence).

XX Sequence 549 AA;

Query Match 31.5%; Score 307.5; DB 19; Length 549;
Best Local Similarity 46.1%; Pred. No. 3e-24;

Matches 59; Conservative 31; Mismatches 37; Indels 1; Gaps 1;

Qy 54 KDRFNDEIDKLTGYKTKSLCMTPIRSSDGEIIGVQAQAIN-KIPEGAPFTEDEKVMQY 112
Db 247 EDPRENAEVDQITGYKTSILCMTPIKHNREEVGVQAQAINKSGNGTFTTEKDEKDFRAY 306

Qy 113 LPFGCIATSNALQFAASRKEYERSRALLEVVDLFEQOTDLEKIVKIMHRAQTLLKCR 172
Db 307 LAFCGIVLHNAQLYETSLLENKRNQVLLDASLIFEEOQSLEVLILKTAATIIISFMQVQK 366

Qy 173 CSQLLED 180

Db 367 CTIFIVDE 374

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:44:04 ; Search time 12.8155 Seconds
(without alignments)

3119.127 Million cell updates/sec

Title: US-09-663-542-1_COPY_1_194

Perfect score: 975

Sequence: 1 MLKQARRPLFRNLSATQWK.....VLLLEDIESPVVFKTKSFEL 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	684	4 Q9GZY7	Q9gy7 homo sapien
2	882	90.5	685	11 Q8VID7	Q8vid7 rattus norv
3	813	83.4	988	4 Q96S76	Q96s76 homo sapien
4	709	72.7	934	4 Q9HCR9	Q9hcr9 homo sapien
5	705	72.3	935	11 Q8VID6	Q8vid6 rattus norv
6	433	44.4	581	11 Q8VID8	Q8vid8 rattus norv
7	429	44.0	576	4 Q9HB46	Q9hb46 homo sapien
8	354.5	36.4	1018	5 Q95TW8	Q95tw8 drosophila
9	354.5	36.4	1232	5 Q9VFI9	Q9vfi9 drosophila
10	349	35.8	1284	5 Q9GVJ79	Q9gvj79 drosophila
11	203	20.8	930	5 Q9GQ06	Q9gq06 trypanosoma
12	201	20.6	836	11 Q8R0D4	Q8rod4 mus musculus
13	201	20.6	861	11 Q91Z01	Q91zq1 mus musculus
14	199	20.4	930	5 Q8WQX9	Q8wx9 trypanosoma
15	189.5	19.4	819	5 Q96076	Q96076 ephydatia f
16	186	19.1	490	4 Q9NY45	Q9ny45 homo sapien

17	185	19.0	861	13 Q8UUY5	Q8uuy5 rana pipien
18	183	18.8	692	6 Q97746	Q97746 canis famil
19	183	18.8	856	6 Q9MYV0	Q9myv0 canis famil
20	181.5	18.6	857	13 Q8UUY6	Q8uuy6 rana pipien
21	181.5	18.6	866	13 Q8UUY7	Q8uuy7 rana pipien
22	180	18.5	800	11 Q62037	Q62037 mus musculu
23	178.5	18.3	860	2 P94182	P94182 anabaena sp
24	178.5	18.3	860	16 Q8YVS0	Q8yvs0 anabaena sp
25	174.5	17.9	859	16 P94181	P94181 anabaena sp
26	165	16.9	657	4 Q9NTV4	Q9ntv4 homo sapien
27	165	16.9	714	4 Q9HCP9	Q9hcp9 homo sapien
28	165	16.9	779	11 Q9WV11	Q9wv11 mus musculu
29	165	16.9	788	11 Q9QYJ5	Q9qyj5 rattus norv
30	165	16.9	789	4 Q9ULW9	Q9ulw9 homo sapien
31	165	16.9	794	11 Q9QYJ6	Q9qyj6 rattus norv
32	164.5	16.9	485	5 Q9GTN9	Q9gtn9 trypanosoma
33	129	13.2	944	16 Q8YV44	Q8yv44 anabaena sp
34	118.5	12.2	445	2 Q9FSY4	Q9fsy4 anabaena va
35	118.5	12.2	1245	5 Q96195	Q96195 plasmodium
36	118.5	12.2	1850	16 Q8YVG4	Q8yvg4 anabaena sp
37	117	12.0	101	4 Q9UD49	Q9ud49 homo sapien
38	117	12.0	773	2 Q9XBM4	Q9xbm4 myxococcus
39	116	11.9	1900	16 Q8YN83	Q8yn83 anabaena sp
40	111.5	11.4	573	16 Q53473	Q53473 mycobacteri
41	104	10.7	235	11 Q9QYT5	Q9qyt5 rattus norv
42	95	9.7	1808	16 Q8YZY1	Q8zy1 anabaena sp
43	94.5	9.7	578	16 P95194	P95194 mycobacteri
44	94	9.6	540	17 Q971R4	Q971r4 sulfolobus
45	94	9.6	1777	16 Q9L708	Q9l708 anabaena sp

ALIGNMENTS

RESULT 1

Q9GZY7 ID Q9GZY7 PRELIMINARY; PRT; 684 AA.
AC Q9GZY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CAMP/CGMP cyclic nucleotide phosphodiesterase IIA3 (Phosphodiesterase IIA2).
DE PDE1IA3 OR HSPDE1IA.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN MEDLINE=20524097; PubMed=11050148;
RX Hetman J.M., Robas N.M., Baxendale R., Fidock M., Phillips S.C., Soderling S.H., Beavo J.A.;
RT "Cloning and characterization of two splice variants of human phosphodiesterase IIA.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20524097; PubMed=11050148;
RA Hetman J.M., Robas N.M., Baxendale R., Fidock M., Phillips S.C., Soderling S.H., Beavo J.A.;
RT "Cloning and characterization of two splice variants of human phosphodiesterase IIA.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=20469516; PubMed=10906126;
RA Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
RT "Isolation and Characterization of Two Novel Phosphodiesterase PDE1IA Variants Showing Unique Structure and Tissue-specific Expression.";
RL J. Biol. Chem. 275:31469-31479(2000).
DR EMBL; AJ278682; CAC15567.1; -;
DR EMBL; AB038041; BAB16372.1; -;
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pelase_Hdc.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.

```
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 684 AA; 78133 MW; 1E41C4F5199D6B1E CRC64;

Query Match 100.0%; Score 975; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 3.8e-74;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQARRPLFRNVLSATQWKVKITRLVQISGASLAEOKEKHQDFLIQRTKTKDRRND 60
DB 1 MLQARRPLFRNVLSATQWKVKITRLVQISGASLAEOKEKHQDFLIQRTKTKDRRND 60
QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
DB 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
QY 121 SNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
DB 121 SNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
QY 181 IESPVVKFTKSFEL 194
DB 181 IESPVVKFTKSFEL 194

RESULT 2
Q8VID7 PRELIMINARY; PRT; 685 AA.
AC Q8VID7;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A3.
GN RNPDE11A3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
(pDE11A): comparison of rat and human pDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059361; BAB79628.1;
DR EMBL; AB048416; BAB62713.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_please_Hdc.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 685 AA; 78067 MW; 505E8748E9A6C21F CRC64;

Query Match 90.5%; Score 882; DB 11; Length 685;
Best Local Similarity 90.7%; Pred. No. 2.8e-66;
Matches 176; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MLQARRPLFRNVLSATQWKVKITRLVQISGASLAEOKEKHQDFLIQRTKTKDRRND 60
DB 1 MLQARRPLFRNVLSATQWKVKITRLVQISGASLAEOKEKHQDFLIQRTKTKDRRND 60
QY 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
DB 61 EIDKLTGYTKSLLCMPIRSSDGEIIGVAQAINKIPEGAPFTEDEKVMQMYLPFCGIAI 120
QY 121 SNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
DB 121 SNAQLFAASRKEYERSRALLEVVNDLFEQTDLEKIVKIMHRAQTLKRCRCSVLLED 180
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QY 181 IESPVVKFTKSFEL 194
DB 181 IESPVVKFTKSFEL 194

RESULT 3
Q96S76 PRELIMINARY; PRT; 988 AA.
ID Q96S76;
AC Q96S76;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase pDE11A gene:
Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB048423; BAB62713.1;
DR EMBL; AB048402; BAB62713.1; JOINED.
DR EMBL; AB048403; BAB62713.1; JOINED.
DR EMBL; AB048404; BAB62713.1; JOINED.
DR EMBL; AB048405; BAB62713.1; JOINED.
DR EMBL; AB048406; BAB62713.1; JOINED.
DR EMBL; AB048408; BAB62713.1; JOINED.
DR EMBL; AB048409; BAB62713.1; JOINED.
DR EMBL; AB048410; BAB62713.1; JOINED.
DR EMBL; AB048411; BAB62713.1; JOINED.
DR EMBL; AB048412; BAB62713.1; JOINED.
DR EMBL; AB048413; BAB62713.1; JOINED.
DR EMBL; AB048414; BAB62713.1; JOINED.
DR EMBL; AB048415; BAB62713.1; JOINED.
DR EMBL; AB048416; BAB62713.1; JOINED.
DR EMBL; AB048417; BAB62713.1; JOINED.
DR EMBL; AB048418; BAB62713.1; JOINED.
DR EMBL; AB048419; BAB62713.1; JOINED.
DR EMBL; AB048420; BAB62713.1; JOINED.
DR EMBL; AB048421; BAB62713.1; JOINED.
DR EMBL; AB048422; BAB62713.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 988 AA; 111170 MW; 7F678869353DF7EB CRC64;

Query Match 83.4%; Score 813; DB 4; Length 988;
Best Local Similarity 39.0%; Pred. No. 2.9e-60;
Matches 194; Conservative 0; Mismatches 0; Indels 304; Gaps 1;

QY 1 MLQARRPLFRNVLSATQWKVKITRLVQISGASLAEOKEKHQDFLIQRTKTK----- 54
DB 1 MLQARRPLFRNVLSATQWKVKITRLVQISGASLAEOKEKHQDFLIQRTKTKMAASRL 60
QY 55 ----- 54
DB 61 DGEVETFLDRHPELFDLYLMRKQEWKVLQRHSQOGALGPRPSLAGTSSLAHSTC 120
QY 55 ----- 54
DB 121 RGGSSVGGGTGPNGSAHSQPLPGGDCGVPSPSWAGSGRGDGNLQRRASOKELRKSEA 180
QY 55 ----- 54
DB 181 RSKATHVNTYDEQVTSRAQEPPLSSVRRALLRKASSLPPTTAHLSALLSRSVNLPOYP 240
QY 55 ----- 54
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Db 241 PTAIDYKCHLKKHNEROFFLELVKDISNDLDTLSYSKILIFVCLMVDADRCSLFVEGA 300
Qy 55 -----DR 56
Db 301 AAGKTLVSKFFDVHAGTLPPLPCSSSENSNEVQPGCKGIIGYVGEHGETVNPIDAYQDR 360
Qy 57 RFNDEIDKLTGYKTKSLLCMPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYLPFC 116
Db 361 RFNDEIDKLTGYKTKSLLCMPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYLPFC 420
Qy 117 GIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCRC 176
Db 421 GIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCRC 480
Qy 177 LLEDIESPVVKFTKSFEL 194
Db 481 LLEDIESPVVKFTKSFEL 498

RESULT 4
Q9HCR9
ID Q9HCR9 PRELIMINARY; PRT; 934 AA.
AC Q9HCR9;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A (Phosphodiesterase 11A4).
GN HSPDE11A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=20469516; PubMed=10906126;
RA Yuasa K., Kotera J., Fujishige K., Michibata H., Sasaki T., Omori K.;
RT "Isolation and Characterization of Two Novel Phosphodiesterase PDE11A
RT Variants Showing Unique Structure and Tissue-specific Expression.";
RL J. Biol. Chem. 275:31469-31479(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570133; PubMed=1121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene:
RT Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB036704; BAB16371.1; -.
DR EMBL; AB048423; BAB62712.1; -.
DR EMBL; AB048403; BAB62712.1; JOINED.
DR EMBL; AB048404; BAB62712.1; JOINED.
DR EMBL; AB048405; BAB62712.1; JOINED.
DR EMBL; AB048406; BAB62712.1; JOINED.
DR EMBL; AB048408; BAB62712.1; JOINED.
DR EMBL; AB048409; BAB62712.1; JOINED.
DR EMBL; AB048410; BAB62712.1; JOINED.
DR EMBL; AB048411; BAB62712.1; JOINED.
DR EMBL; AB048412; BAB62712.1; JOINED.
DR EMBL; AB048413; BAB62712.1; JOINED.
DR EMBL; AB048414; BAB62712.1; JOINED.
DR EMBL; AB048415; BAB62712.1; JOINED.
DR EMBL; AB048416; BAB62712.1; JOINED.
DR EMBL; AB048417; BAB62712.1; JOINED.
DR EMBL; AB048418; BAB62712.1; JOINED.
DR EMBL; AB048419; BAB62712.1; JOINED.
DR EMBL; AB048420; BAB62712.1; JOINED.
DR EMBL; AB048421; BAB62712.1; JOINED.
DR EMBL; AB048422; BAB62712.1; JOINED.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR Pfam; PF01590; GAF; 2.

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DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 934 AA; 104810 MW; 994675824259447E CRC64;

Query Match 72.7%; Score 709; DB 4; Length 934;
Best Local Similarity 99.3%; Pred. No. 1.7e-51;
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 54 KDRFNDEIDKLTGYKTKSLLCMPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 304 QDRFNDEIDKLTGYKTKSLLCMPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 363
Qy 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCRC 173
Db 364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCRC 423
Qy 174 SVLLEDIESPVVKFTKSFEL 194
Db 424 SVLLEDIESPVVKFTKSFEL 444

RESULT 5
Q9VID6
ID Q9VID6 PRELIMINARY; PRT; 935 AA.
AC Q9VID6;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Phosphodiesterase 11A4.
GN RNPDE11A4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohgaru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
RT (PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059362; BAB79629.1; -.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 935 AA; 104570 MW; E80F1039770F8276 CRC64;

Query Match 72.3%; Score 705; DB 11; Length 935;
Best Local Similarity 97.9%; Pred. No. 3.6e-51;
Matches 138; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 54 KDRFNDEIDKLTGYKTKSLLCMPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 113
Db 304 QDRFNDEIDKLTGYKTKSLLCMPIRSDGIIIGVAQAINKIPGAPTEDEKVMQMYL 363
Qy 114 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCRC 173
Db 364 PFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLLKCRC 423
Qy 174 SVLLEDIESPVVKFTKSFEL 194
Db 424 SVLLEDIESPVVKFTKSFEL 444

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RESULT 6
Q8VID8      PRELIMINARY;          PRT;      581 AA.
AC Q8VID8:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Phosphodiesterase 11A2.
GN RNPDE11A2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21393948; PubMed=11502204;
RA Yuasa K., Ohguru T., Asahina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
RT (PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Eur. J. Biochem. 268:4440-4448(2001).
DR EMBL: AB059360; BAB79627.1; -
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
SQ SEQUENCE 581 AA; 66141 MW; 2CA7C2F5DDB37D00 CRC64;

Query Match      44.4%; Score 433; DB 11; Length 581;
Best Local Similarity 100.0%; Pred. No. 1.9e-28;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 VQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVDLFEQTDLEKIVKKIMHRAQTL 167
Db 4 VQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVDLFEQTDLEKIVKKIMHRAQTL 63
QY 168 LKCRCSVLLLEDIESPVVKTKSPFL 194
Db 64 LKCRCSVLLLEDIESPVVKTKSPFL 90

RESULT 7
Q8HB46      PRELIMINARY;          PRT;      576 AA.
AC Q8HB46:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CAMP/cGMP phosphodiesterase 11A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=TESTIS;
RX MEDLINE=20524097; PubMed=11050148;
RA Hetman J.M., Robas N., Baxendale R., Fidock M., Phillips S.C.,
RA Soderling S.H., Beavo J.A.;
RT "Cloning and characterization of two splice variants of human
RT phosphodiesterase 11A.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12891-12895(2000).
DR EMBL; AF281865; AAG32023.1; -
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
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DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 576 AA; 65766 MW; 3992C4C95A5B0B36 CRC64;

Query Match      44.0%; Score 429; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 4.2e-28;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVDLFEQTDLEKIVKKIMHRAQTL 168
Db 1 MQMYLPFCGIAISNAQLFAASRKEYERSRALLEVVDLFEQTDLEKIVKKIMHRAQTL 60
QY 169 KCERCSVLLLEDIESPVVKTKSPFL 194
Db 61 KCERCSVLLLEDIESPVVKTKSPFL 86

RESULT 8
Q95TW8      PRELIMINARY;          PRT;      1018 AA.
AC Q95TW8:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE GH27433p.
GN CG8279.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J.E., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.W., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY058470; AAL13699.1; -
DR FlyBase; FBgn0038237; CG8279.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase; 1.
DR PROSITE; PS00126; PDEASE_I; UNKNOWN_1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 1018 AA; 114668 MW; 8C758A607855EDD9 CRC64;

Query Match      36.4%; Score 354.5; DB 5; Length 1018;
Best Local Similarity 44.8%; Pred. No. 1.6e-21;
Matches 82; Conservative 23; Mismatches 55; Indels 23; Gaps 3;

QY 28 VOISGASLAEOEKHQDFLIQRTKDRRENDEIDKLTGYTKSLLOMCPIRSSDGEIIG 87
Db 213 IGIAGMVAQTQKQ-----MINIKAYKDARENCEIDKLTGYTKNALCMPICNYEGDIIG 266
QY 88 VQAQINKIPEGAPFETDEKVMQVLPFCGIAISNAQLFAASRKEYERSRALLEVVDLF 147
Db 267 VQAQINKTNGCMFEHDHVEIFRRYLTFCGIGIQNAQLFEMSVOEYRNNILLNARSIF 326
QY 148 EEQTDLEKIVKKIMHRAQTLKCRCSVLLLE-----DIESP-----VVKTK 190
Db 327 EEQNNECLVTKIMTEARELLKCRCSVFLVDLDCCEASHLEKIEKPNQPATRAIKSAD 386
QY 191 SFE 193
Db 387 SFE 389
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RESULT 9
Q9VFI9
ID Q9VFI9 PRELIMINARY: PRT: 1232 AA.
AC Q9VFI9
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CG8279 protein.
GN CG8279.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glödek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nixon K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003705; AAF5066.2;
DR FlyBase; FBgn0038237; CG8279.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PD1ESTERASE1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDASE_I; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 1232 AA; 137426 MW; ECF6B9C3A71BAF74 CRC64;

Query Match 36.4%; Score 354.5; DB 5; Length 1232;
Best Local Similarity 44.8%; Pred. No. 2.1e-21;

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Matches 82: Conservative 23; Mismatches 55; Indels 23; Gaps 3;
QY 28 VOISGSLAEKQKHQDFLIQRTKTKDRFRNDEIDKLTGYTKTSLLCLMPRSSDGLIG 87
DB 326 IGIAGMVAQTKQ-----MINIKAYKQARENCEIDLTKYKTNAILCMPICNVEGDIIG 379
QY 88 VAQAINKIPEGAPFTEDDEKVMQMYLPFCGTAISNAQLFAASRKYEYSRALLLEVNDLF 147
DB 380 VAQIINKTNGCMFEDEHVEIFRRLYTFCGIGIQNAQLFEMSVQYRRNQLILNARSIF 439
QY 148 EEOTDLEKIVKIMHRAOTLLKRCRCSVLLLE-----DIESP-----VVKFTK 190
DB 440 EEQNNECLVTIKMFEARELLKRCRCSVFLVDLDCCEASHLEKIITEKPNQATRAIKSAD 499
QY 191 SFE 193
DB 500 SFE 502

RESULT 10
Q9VJ79
ID Q9VJ79 PRELIMINARY: PRT: 1284 AA.
AC Q9VJ79
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CG10231 protein.
GN CG10231.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glödek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nixon K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003705; AAF5066.2;
DR FlyBase; FBgn0038237; CG8279.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; ME_Pplase_HDC.
DR InterPro; IPR002073; PDase.
DR InterPro; IPR001230; Prenyl_site.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PD1ESTERASE1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDASE_I; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 1232 AA; 137426 MW; ECF6B9C3A71BAF74 CRC64;

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"The genome sequence of Drosophila melanogaster.";

RT Science 287:2185-2195(2000).
 DR EMBL: AE003659; AAF53675.1; .
 DR FlyBase: FBgn0032686; CG10231.
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR003607; ME_Pplase_Hdc.
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 DR Pfam: PF01590; GAF; 2.
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 DR SMART: SM00065; GAF; 2.
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 SQ SEQUENCE 1284 AA; 141726 MW; F6873C90A9953430 CRC64;

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OY 20 KKVITRLVQISGASLAQKQKHQDFLIQROT-----KTKDRRFNDEI 62
 DB 263 KKLVSKLFDVCPRTVEEMQODEVRVWGTGIAGHVAESGEPVNPIDAYQDERFNCI 322
 OY 63 DKLGYTKYKSLLCMPIRSDDGEIIGVQAQINKIPEGAPFTTDEKVMQMYLPFCGIAISN 122
 DB 323 DSLGYRTKALLCPIKIDSGDVIGVAQVINKM-NGECFSEIDKVFSSYLQFCGIGLRN 381
 OY 123 AOLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLKLCERCVSLLLEDIE 182
 DB 392 AOLKESOLEIKRNOVLDLARMIFEQSTIEHVMVFRILTHMQSLQCORVOILLVHEAD 441
 OY 183 SPVVKFTKSF 193
 DB 442 KG--SFSRVFD 450

RESULT 11

ID Q9GQ06 PRELIMINARY; PRT; 930 AA.
 AC Q9GQ06; 01-MAR-2001 (TremBLrel. 16, Created)
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Cyclic nucleotide phosphodiesterase.
 GN PDE.
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rascon A., Soderling S.H., Beavo J.A.;
 RT "Cloning and characterization of a cyclic nucleotide phosphodiesterase
 from Trypanosoma brucei."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF192755; AAG43461.1; .
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR003607; ME_Pplase_Hdc.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: PF01590; GAF; 2.
 DR Pfam: PF00233; PDEase; 1.
 DR PRINTS: PR00387; PDIESTERASE1.
 DR SMART: SM00065; GAF; 2.
 DR SMART: SM00471; Hdc; 1.
 DR PROSITE: PS00126; PDEASE_I; 1.
 SQ SEQUENCE 930 AA; 103269 MW; 4E297F6347F59A29 CRC64;

Query Match 20.8%; Score 203; DB 5; Length 930;

Best Local Similarity 35.3%; Pred. No. 9.3e-09;

Matches 48; Conservative 31; Mismatches 43; Indels 14; Gaps 4;

OY 55 DRRENDEIDKLTGYTKSLLCMPIRSDDGEIIGVQAQINK-----IPEGAPFTD 104
 DB 302 DDRFNREVDKATGYRTKILCMPV-MYEGTIVAAQLINKLDLTSTESGLRLPR--VFGR 358

OY 105 DEKVMQMYLPFCGIAISNAQLFAASRKEYERSRALLEVNDLFE-EQTDLEKIVKIMHR 163
 DB 359 DEELFQTFSEFAGASLNCRINDRLLEKKKSDVILDVVTLSNTDTRDVGIVRHALHG 418
 OY 164 AOTLLKERCVSLLLE 179
 DB 419 AKLLNADRSTLFLVD 434

RESULT 12

ID Q8R0D4 PRELIMINARY; PRT; 836 AA.
 AC Q8R0D4;
 DT 01-JUN-2002 (TremBLrel. 21, Created)
 DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Similar to phosphodiesterase 6C, CGMP specific, cone, alpha
 DE prime.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC027050; AAH27050.1; .
 SQ SEQUENCE 836 AA; 95906 MW; A8D60FAAFE6C9D9E CRC64;

Query Match 20.6%; Score 201; DB 11; Length 836;

Best Local Similarity 37.8%; Pred. No. 1.2e-08;

Matches 48; Conservative 26; Mismatches 49; Indels 4; Gaps 3;

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 OY 113 LPFCGIAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKIMHRAQTLKCCR 172
 DB 217 LSFVAVALRQHTSYLSVESRRSQILMWSANKVFEELTDVERQFHKALYTIRTYLNCDR 276
 OY 173 CSVLLLE 179
 DB 277 YSIGLLD 283

RESULT 13

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 AC Q91ZQ1;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
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 GN PDE6C
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=RETINA;
 RA Chang B., Hawes N.L., Hurd R.E., Davisson M.T., Nusinowitz S.,
 RA Heckenlively J.R.;
 RT "A sequence alteration in Pde6c gene causes cone photoreceptor
 function loss (cpfl1) in mice."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF411063; AAK96254.1; .
 DR MGD: MGI:105956; Pde6c.
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR002073; PDEase.

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 10:43:55 ; Search time 5414 Seconds
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11170.231 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb_in.*
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- 17: em_hum.*
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- 19: em_mu.*
- 20: em_on.*
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- 35: em_htg_rod.*
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- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2058	99.0	2502	9	HSA278682	AJ278682 Homo sapi
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4	1891.8	91.0	4476	9	AB036704	AB036704 Homo sapi
5	1734.8	83.5	2141	9	AF281865	AF281865 Homo sapi
6	1684	81.0	3492	10	AB059361	AB059361 Rattus no
7	1551.4	74.7	4170	10	AB059362	AB059362 Rattus no
8	1503.8	72.4	1784	9	HSA251509	AJ251509 Homo sapi
9	1414.4	68.1	3098	10	AB059360	AB059360 Rattus no
10	1007.4	48.5	2083	9	AK074273	AK074273 Homo sapi
11	417.8	20.1	5687	3	AX122262	AX122262 Drosophill
12	388.8	18.7	426	6	AX375673	AX375673 Sequence
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14	356.6	17.2	2499	6	E52149	E52149 Novel prote
15	356.6	17.2	2645	6	AX036123	AX036123 Sequence
16	356.6	17.2	2645	6	I58538	I58538 Sequence 22
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18	356.6	17.2	3106	9	AF043731	AF043731 Homo sapi
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30	345.2	16.6	1982	6	I87003	I87003 Sequence 12
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ALIGNMENTS

RESULT 1
AX139462
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX139462
Sequence 2 from Patent EP1085089.
AX139462
AX139462.1 GI:14275107

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2078)

Fidock,M.D. and Kobas,N.M.

Human cyclic nucleotide phosphodiesterase

Patent: EP 1085089-A 2 21-MAR-2001;

JOURNAL

Pfizer Limited (GB) ; PFIZER INC. (US)			
FEATURES	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
BASE COUNT	615 a 439 c 491 g 533 t		
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Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2078; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1 GGTCCGAGATGCTGAAGCAGGCAGAGACGCTTTATTTCAGAAATGTGCTCAGTGCCACAC	60	
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Db	61 ACTGGAAAAGGTGAAAATCACAAAGCTGGTCCAAATCTCTGGGGCCCTCTTTGGCTGAAA	120	
QY	121 AACAGGAAAAGCCAGGATTTTCTTATACAGAGGCAAAACAAACAAAGGATCGACGAT	180	
Db	121 AACAGGAAAAGCCAGGATTTTCTTATACAGAGGCAAAACAAACAAAGGATCGACGAT	180	
QY	181 TCAATGATGAATCGACAAGCTGACTGGATACAGACAAATCAATATTGTGATGCCTA	240	
Db	181 TCAATGATGAATCGACAAGCTGACTGGATACAGACAAATCAATATTGTGATGCCTA	240	
QY	241 TCCGAAGCAGTGATGGTGAGATTAATGGTGGCCCCAAGCGATAAATAAGATTCCCTGAAG	300	
Db	241 TCCGAAGCAGTGATGGTGAGATTAATGGTGGCCCCAAGCGATAAATAAGATTCCCTGAAG	300	
QY	301 GAGCTCCATTACTGAAGATGATGAAGAGTAAAGATTAATGACAGATGATCTTCCATTGTGGAA	360	
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Db	1201	GTAGGTGGCTTTTACACAGTGAGGAAAACATATCGATGGTTCTATACCAACTGGAGAC	1260
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Qy	1321	TTCTGACCCGAGGTGGAAATTTTAGCGGTGATTTGGGGATGCTGTGATGACCTCGACC	1380
Db	1321	TTCTGACCCGAGGTGGAAATTTTAGCGGTGATTTGGGGATGCTGTGATGACCTCGACC	1380
Qy	1381	ACAGGGAAACCAACATGCTTCCAAAGCTAAGAGTGGCTCTGCCCTGGCCCAACTCTATG	1440
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 Db 2060 AAACCTGAAGCCGATGCTAGATTAGTCTAGTCTACAAACAGAGTAACTGGGAAGAGCTACAC 2119
 QY 1986 CAAAACGACTGCTGGCTCAACTGCCTCACTCCTCCCTGCGAGTGTATGTTAGTACCC 2045
 Db 2120 CAAAACGACTGCTGGCTCAACTGCCTCACTCCTCCCTGCGAGTGTATGTTAGTACCC 2179
 QY 2046 AAGGAAGACAGAACTAA 2063
 Db 2180 AAGGAAGACAGAACTAA 2197

RESULT 3
 AB038041
 LOCUS AB038041 3507 bp mRNA linear PRI 06-OCT-2000
 DEFINITION Homo sapiens HSPDELLA mRNA for phosphodiesterase 11A2, complete
 cds.
 ACCESSION AB038041
 VERSION AB038041.1 GI:10716053
 KEYWORDS phosphodiesterase 11A2.

SOURCE Homo sapiens testis cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Yuasa,K., Kotera,J., Fujishige,K., Michibata,H., Sasaki,T. and Omori,K.
 TITLE Isolation and characterization of two novel phosphodiesterase PDE11A variants showing unique structure and tissue-specific expression
 JOURNAL J. Biol. Chem. 275 (40), 31469-31479 (2000)
 MEDLINE 20469516
 REFERENCE 2 (bases 1 to 3507)
 AUTHORS Yuasa,K. and Omori,K.
 TITLE Direct Submission
 JOURNAL Submitted (07-FEB-2000) Kenji Omori, Tanabe Seiyaku Co. Ltd., Discovery Research Laboratory; 2-50 Kawagishi-2-chome, Toda, Saitama 335-8505, Japan (E-mail:k-omori@tanabe.co.jp, Tel:+81-48-433-8069, Fax:+81-48-433-8159)
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2057; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1926 AAACCTGAAGCCGATCTAGATTCAGTACAAACAGAGTAAGTGGGAGAGCTACAC 1985
Db 2017 AAACCTGAAGCCGATCTAGATTCAGTACAAACAGAGTAAGTGGGAGAGCTACAC 2076
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Db 2077 CAAAACGACTGCTGGCTTCAACTGCTCATCTCTCCCTGCCAGTGTATGTTAGGCC 2136
QY 2046 AAGGAAGACAGGAACATAA 2063
Db 2137 AAGGAAGACAGGAACATAA 2154

RESULT 4
AB036704
LOCUS
DEFINITION
AB036704
ACCESSION
VERSION
AB036704.1 GI:10716051
phosphodiesterase 11A.
KEYWORDS
Homo sapiens
Homo sapiens prostate cDNA to mRNA.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
Yusa, K., Kotera, J., Fujishige, K., Michibata, H., Sasaki, T. and
Omori, K.
Isolation and characterization of two novel phosphodiesterase
PDE11A variants showing unique structure and tissue-specific
expression
J. Biol. Chem. 275 (40), 31469-31479 (2000)
2 (bases 1 to 4476)
Omori, K. and Yusa, K.
Direct Submission
Submitted (06-JAN-2000) Keioji Omori, Tanabe Seiyaku Co. Ltd.,
Discovery Research Laboratory; 2-50 Kawagishi-2-chome, Toda,
Saitama 335-8505, Japan (E-mail:k-omori@tanabe.co.jp,
Tel:+81-48-433-8069, Fax:+81-48-433-8159)

FEATURES	Location/Qualifiers		QY	709	TTCCAGTGAACATCAGTGCCTACACAGATCCGCGCTTTGATGCAGAGCCAGACCAGA	768
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BASE COUNT	1260 a 980 c 1109 g 1127 t		Db	2189	TCACAGCTGCTCTCCGGATGTTTCATGGAGCTGGGATGGTACAGAAATTTAAATTTGACT	2248
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QY	169 AGGATCGAGGATTCATGATGAAATCGACAAGCTGACTGGATACAGACAAAATCATAT		QY	1249	ACAACTGGAGACATGCCITTCACAGCTGTGTCAGCTGATGTTCCGCGATGTTAAACACTGCTG	1308
	1229 AGGATCGAGGATTCATGATGAAATCGACAAGCTGACTGGATACAGACAAAATCATAT					
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BASE COUNT 1100 a 1004 c 1067 g 999 t
ORIGIN

Query Match 74.7%; Score 1551.4; DB 10; Length 4170;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 216; Indels 3; Gaps 1;

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DB	1859	ATGACCAAGTGAAGAGCTCTGGGCCAAGCAGTCTGTGGCTTTGATGCTGCTCTTACC	1918
QY	1009	ATGCAACATGTCAAAGCTGAGTTGACAGTTTAAAGCGACCCAAACATCCCTCTGGTGT	1068

RESULT 8
HSA251509

LOCUS HSA251509 1784 bp mRNA linear PRI 23-MAR-2000
DEFINITION Homo sapiens mRNA for cyclic nucleotide phosphodiesterase 11A1
(PDE11A gene).
ACCESSION AJ251509
VERSION AJ251509.1 GI:7327960
KEYWORDS cyclic nucleotide phosphodiesterase 11A1; PDE11A gene.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1784)
AUTHORS Fawcett, L., Baxendale, R., Stacey, P., McGrouther, C., Harrow, I.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Molecular cloning and characterization of a distinct human
phosphodiesterase gene family: PDE11A
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3702-3707 (2000)
MEDLINE 20202699
PUBMED 10725373
REFERENCE 2 (bases 1 to 1784)
AUTHORS Phillips, S.C.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-1999) Phillips S.C., Discovery Biology, Pfizer
Central Research, Ramsgate Road, Sandwich, Kent CT13 9NJ, UNITED
KINGDOM

FEATURES

Location/Qualifiers

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Matches 1505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 9
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DEFINITION Rattus norvegicus RNPDE11A2 mRNA for phosphodiesterase 11A2,
complete cds.
ACCESSION AB059360
VERSION AB059360.1 GI:18143348
KEYWORDS Rattus norvegicus cDNA to mRNA.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1
Yusa,K., Ohguru,T., Asahina,M. and Omori,K.
Identification of rat cyclic nucleotide phosphodiesterase 11A
(PDE11A): comparison of rat and human PDE11A splicing variants
Eur. J. Biochem. 268 (16), 4440-4448 (2001)
21393948
2 (bases 1 to 3098)
Yusa,K. and Omori,K.
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Fax:81-48-433-8159)
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AK074273
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Homo sapiens mRNA for cyclic nucleotide phosphodiesterase 11A1.
AK074273
ACCESSION
VERSION
KEYWORDS
SOURCE
Oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
clone:HEP10314.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
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AUTHORS
Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2. (bases 1 to 2083)
AUTHORS
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.

TITLE
JOURNAL
Direct Submission
Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,
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(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing; Department of Virology and Human
Genome Center, Institute of Medical Science, University of Tokyo
(partly supported by Science and Technology Agency).
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Qy	1729	GGGAGATCTCCAGACAGTGGCAGAACTTCTAACCACTGAGTTCTTCGAAACAAGGAGATC	1788
Db	3739	GGGAGATTGAGAACGCTGGCTGATTTGGTTAGTCGGAGTTTTCGACAGGGAGATA	3798
Qy	1789	GGGAGGATTAGAGCTCAAACTCACTCTTTCAGCAATTTTTTGTGCGAAACCGGAAGGATG	1848
Db	3799	TGGAGAAGCAGGAGCTCAATATAACTCTATTGATATCATGAATCGGAAAGAGGAGCG	3858
Qy	1849	AATGCGCTTCGGTTGCAACTGGAGTGGATGATAGCATCTGCATGCCCTTTCTATCAGGCAC	1908
Db	3859	AGCTGCCCATGATGCAAGTCAACTTTATAGACTCCATTTGCTTGCCCAATCTATGAGCCCT	3918
Qy	1909	TGGTGAAGGTCACAGTCAAACTGAAGCCGATGCTAGATTTCAGTAGCTACAAACAGAGTA	1968
Db	3919	TTGCCACCTCTCCGACAAGCTTGAGCCCTTTGTCGAGGCGTGGCGGATAATTCGAGGCC	3978
Qy	1969	AGTGGGAAGAGCT 1981	
Db	3979	ATTGGATTGATCT 3991	
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AX375673			
LOCUS	AX375673	426 bp	DNA linear PAT 01-MAR-2002
DEFINITION	Sequence 4 from Patent WO200854.		
ACCESSION	AX375673		
VERSION	AX375673.1 GI:19170221		
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Ramakrishnan, S.		
TITLE	Regulation of human phosphodiesterase-like enzyme		
JOURNAL	Patent: WO 0200854-A 03-JAN-2002;		
FEATURES	Bayer Aktiengesellschaft (DE)		
source	Location/Qualifiers		
	1..426		
BASE COUNT	137 a 76 c 94 g 119 t		
ORIGIN	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
Query Match	18.7%; Score 388.8; DB 6; Length 426;		
Best Local Similarity	99.5%; Pred. No. 2.5e-95;		
Matches	390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
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Qy	231	TGCATGCTATCCGAACGATGATGGTGAGATTATGCTGGCCCAAGCGATAAATAAG	290
Db	61	TGCATGCTATCCGAACGATGATGGTGAGATTATGCTGGCCCAAGCGATAAATAAG	120
Qy	291	ATTCTTGAAGGAGCTCCATTACTGAAGATCATGAAAGTTATGACAGATGTATCTTCCA	350
Db	121	ATTCTTGAAGGAGCTCCATTACTGAAGATCATGAAAGTTATGACAGATGTATCTTCCA	180
Qy	351	TTTTTGTGGATCGGCATATCTAAGCTCAGCTCTTTGCTGCCCTCAAGGAAGAATATGAA	410
Db	181	TTTTTGTGGATCGGCATATCTAAGCTCAGCTCTTTGCTGCCCTCAAGGAAGAATATGAA	240
Qy	411	AGAAGCAGACTTTGCTAGAGGTGGTTAATGACCTCTTTCAAGAACAGACTGACCTGGAG	470
Db	241	AGAAGCAGACTTTGCTAGAGGTGGTTAATGACCTCTTTCAAGAACAGACTGACCTGGAG	300
Qy	471	AAAATTGTCAGAAAATTAATGCATCGGGGCCCAAACTCTGCTGAAATGTGAGCGCTGTCT	530

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301 AAAATTGTCAAGAAATATGATCGGCCCAAACTCTGCTGAAATGTCAAGCGTGTCT 360
QY 531 GTTTTACTCCCTAGAGGACATCGAATCACCAGT 562
Db 361 GTTTTACTCCTAGAGGACATCGAATCACCAGT 392

RESULT 13
E52150          2172 bp      DNA      linear      PAT 31-JAN-2002
LOCUS Novel protein and DNA thereof.
DEFINITION E52150
ACCESSION E52150.1 GI:18622238
VERSION JP 2000354492-A/6.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2172)
Taruji.N., Tsuchiya.T. and Nakahama,K.
Novel protein and DNA thereof
Patent: JP 2000354492-A 6 26-DEC-2000;
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
PN JP 2000354492-A/6
PD 26-DEC-2000
PF 19-JUL-1999 JP 1999204336
PR
PI NAKOI TARUI,TAKAYUKI TSUCHIYA,KAZUO NAKAHAMA
PC C12N15/09,C07K16/40,C12N1/21,C12N9/16,C12Q1/34//A61K38/46, PC
A61K38/55,
PC A61K39/395,A61K39/395,(C12N1/21,C12R1:19),(C12N9/16,C12R1:19),
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PC A61K37/54,A61K37/64
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ORIGIN

Query Match 17.2%; Score 356.6; DB 6; Length 2172;
Best Local Similarity 52.0%; Pred. No. 2e-86;
Matches 954; Conservative 0; Mismatches 854; Indels 25; Gaps 6;

QY 169 AGGATCGACGATTAATGATGAATCGACAAGCTGACCTGGATACAAAGACAAAATCATTAT 228
Db 287 AGGATCTCGGTTCAATGCAGAGTTGACCAAAATTACAGGCTACAGACACAAAGCAATTC 346
QY 229 TGTGATCGCCTATCCGAAGCAGTGTGATGATTAATTTGGTGCCCAAGCAGATAAATA 288
Db 347 TTTGTATGCCAATTAAAGAAATCATAGGAAGAGTTGTTGGTGTACGCCAGGCCATCAACA 406
QY 289 AGATTCCCTG---AAGGACCTCAATTACTGAAGATGCAAAAAGTTATGAGATGTATC 345
Db 407 AGAAATAGGAAACGGTGGGACATTACTGAAAAGATGAAAAGGACCTTTGCTGCTTATT 466
QY 346 TTCCATTTTGTGGAATCGCCATATCTAACGCTCAGCTCTTTGCTGCCCTCAAGGAAGAAAT 405
Db 467 TGGCATTTTGGTATTTGTTCTCATATGCTCAGCTCTATGAGACTTCATCTGCTGGAGA 526
QY 406 ATGAAGAACAGCAGCTTTTGTGTAGAGTGGTTAATGACCTCTTTGAAGAACAGACTGACC 465
Db 527 ACAAGAGAAATCAGGTGCTGCTGACCTTGTGAGTTTAATTTTGAAGAACAAACATCAT 586
QY 466 TGGAGAAATTTCTCAAGAAATAATGCAATCGGCCCAAACTCTGCTGAATGTGAGCGCT 525
Db 587 TAGAAGTAATTTGAAGAAATAATAGTGCCTATTTATCTCTTTTCAAGTGCAGAAAT 646
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QY 526 GTTCTGTTTTTACTCTCTAGAGGACATCGAATCACCAGTGTGTAATTTTACCAAAATCCTTTG 585
Db 647 GCACCACTTTTCATAGTGGATGAAGATTGCTCCGATTCTTTTCTAGTGTGTTTCATCG 706
QY 586 AATTGATGTCGCCAAAGTGCGAGTGTGATGCTGAGAACAGTTTCAAGAAAGCATGGAGA 645
Db 707 AGTGTGAGGAATTTAGAAAAATCATCTGATACATTAACAAGGGAACATGTCNAACAAA 766
QY 646 AATCATCATCTCCACTGGCTTAATAAATACAGCATTTGCTGAGCTGGTGTCTTCAACAG 705
Db 767 TCAATTACATGTATGCTCAGTATGTCAAAAATACTATGAAACCACTTAATATCCAGATG 826
QY 706 GCCTTTCCAGTGAACATCAGT-----GATGCCCTTACCAGGATCGCCCTTTGATGCAGAGC 760
Db 827 TCAGTAAGATAAAGAGATTTCCTTGGACAACACTGAAATATACAGGAATATGAACACAGCAGT 886
QY 761 AGACAGATATCTGTTTTCATATAAGATCTGTTCTTTGTGTCCTATTTTGAATATAGCAA 820
Db 887 GCATTAGAAGTTTGTCTTTGTACACCTATAAAAAATGGAAGAAAGAAATAAAGTTATAGGGG 946
QY 821 CCACCAATAATTTGAGTGGCTCAAGTGTAAACAGACTTGTATGGAAACCTTTTGTATGA 880
Db 947 TTTGCCAACTTGTTAATAAGATGGAGAGAAATACTGGC--AAGGTTAAGCCCTTTCAACCG 1004
QY 881 TGCAGATCAACGACTTTTGTGAGGCTTTTGTCTCATCTTTTGTGGACTTGGCATCAACAAC 940
Db 1005 AAATGACGAACAGTTTCTGGAAGCTTTTGTCTCATCTTTTGTGGTGGGATCCCAACAC 1064
QY 941 AATTATGATGATCAAGTGAAGAACTCTGGGCCAAGCAGTCTGTGGCTTTGTATGATGCT 1000
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QY 1001 ATCATACCATGCAACATGTTCAAAAGCTTGAAGTTTCAAGTTTAAGGACGCCAACATCCC 1060
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QY 1061 TCTGGTGTCA-----GAACTTGCATCGATGACATTCATTTTGTATGACTTTCTCTCT 1111
Db 1185 TGTGTCATCTGCCAGACCCCTTAAATTTACTGACTTTAGCTTCACTGACTTTGAGCT 1244
QY 1112 CGAGTGTGATGCCATGATCACAGCTGCTCTCCGATGTTTCATGAGCTGGGATGGTACA 1171
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QY 1172 GAAATTTAAATTTGACTATGAGACACTGTGTAGGTGGCTTTTGGACAGTGGAGAAAAC 1231
Db 1305 GAACCTCCAGATGAACATGAGGTTCTTTGAGATGAGATTTTAAAGTGTAAAGAAATA 1364
QY 1232 TCGGATG---GTTCTTATACCACAACTGGAGACATGCTTCAACGTTGTGCTGAGCTGAT 1288
Db 1365 TCGGAGAAATGTTGCCCTATCATATTTGAGACATGCCCCTTTAATACAGCTCAGTGCAT 1424
QY 1289 CGCGATGTTAACTGCTGGGTTTCAAGACATTTCTGACCGAGGTGGAAATTTTACGGGT 1348
Db 1425 TGCTGCTCTAAAGCAGGCAAAATTCAGAACAAAGCTGACTGACCTGGAGACTTTGCATT 1484
QY 1349 GATTGTGGATGCTGCTGTCATGACCTCGACCAAGGGAACCAACATGCTTCCAAGC 1408
Db 1485 GCTGATTGCTGCATTAAGCCACGATTTGGATCACCCTGTTGTAATACTCTTATACATA 1544
QY 1409 TAAGATGGCTCTGCTGCTGGCCCAACTCTATGGAACCTCTGCTACCTTTGGAGCATCACA 1468
Db 1545 GCGAAGTGAACATCCACTTGGCCAGCTTTACTG---CCATTCATCATGGAACACATCA 1601
QY 1469 TTTCAACCAAGCGGTGATGATCCTTCAAGTGAAGGTGCACATATCTTTTGTAACTGTC 1528
Db 1602 TTTTGACCAAGCTGATGATGATTTAATAGTCCAGGCAATCAGATCTCAGTGGCTCTC 1661
QY 1529 CTCCAAGAAATATAGTGACCTTTATGACCTTTTGAAGCAGTCAATATTTGGCAACAGCT 1588
Db 1662 CATTAAGAAATATAGACCAAGCTTTGAANAATTAATCAAGCAAGCTATTTTAGCTACAGCT 1721
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Query Match	17.2%	Score 356.6;	DB 6;	Length 2499;
Best Local Similarity	52.0%;	Pred. No. 2e-86;		
Matches 954;	Conservative 0;	Mismatches 854;	Indels 25;	Gaps 6;
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Qy	229	TGTGCAATGCCCTATCCGAAGCAGTGATGCTCAGATATTGTGTGGCCCAAGCGATAAATA	288
Db	674	TTTGTATGCCAAATTAGAATCATAGGGAAGAGTTGTGTGTAGCCAGGCCATCAACA	733
Qy	289	AGATTCTGCT---AAGGAGCTCCATTACTGAAGATGATGAAAAAGTTATGCGATGTATC	345
Db	734	AGAAATCAGGAAACGGTGGGACATTTACTGAAAAGATGAAAAGGACTTTGCTGCTTATT	793
Qy	346	TTCCATTTTTGTGAAATGCCCATATCATACGCTCAGCTCTTTGCTGCGCTCAAGGAAGAAT	405
Db	794	TGGCATTTTGTGTAATGTTCTTCATAACTCTCAGCTCTATGAGACTTTCTACTGCTGGAGA	853
Qy	406	ATGAAAGAAGCAGAGCTTTGCTAGAGTGTGTAATGACCTTTTGAAGAAGACAGACTGACC	465
Db	854	ACAAGAGAATCAGGTGCTGCTTGACCTTCTAGTTTAATTTTGAAGACAACAATCAT	913
Qy	466	TGGAGAAAAATTGTCAAGAAAAATATGCATCGGCCCAACTCTGCTGAAATGTGAGCGCT	525
Db	914	TAGAAGTAATTTGAAGAAAAATAGTCCCACTATTATCTCTTTCATGCAAGTGCAGAAAT	973
Qy	526	GTTCGTGTTTACTTCCTAGAGAGCATCGAATCACCAAGTGGTGAATTTACCAAAATCCTTTG	585
Db	974	GCACCATTTTCATAGTGGATGAAGATTGCTCCGATCTCTTTCTAGTGTGTTTCACATGG	1033
Qy	586	AATTGATGTCCTCCAAAGTCAGTGCATGCTGAGAACAGCTTTCAAAGAAGATGCAGA	645
Db	1034	AGTGTGAGGAATTTAGAAAAATCATCTGATACATTTACAAGGGAACATGATGCAAAACAAA	1093
Qy	646	AATCATCATACTCCGACTGGCTAATAAATAACAGCAATGCTGAGCTGGTTGCTTCAACAG	705
Db	1094	TCAATTACATGTATGCTCAGTATGTCAAAAATACTATGGAACCCACTTAATATCCCAGATG	1153
Qy	706	GCCTTCAGTGAACATCAGT-----GATGCTACCGAGGATCCGGCTTTGATGCGAGAGC	760
Db	1154	TCAGTAAGGATAAAGATTTTCCCTGGACAACTGAAAAATACAGGAAAAATGTAACCCAGCAGT	1213
Qy	761	AGACCAGATATCTGGTTTTCACATAAGATCTGTTCTTTGTGTCCTATTTTGGGAATAGCAA	820
Db	1214	GCATTAGAAGTTGCTTTGTACACCTATAAAAAATGGAAGAAGATAAAGTTATAGGGG	1273
Qy	821	CCACCAAAATAATTGGAGTGGCTCAAGTGTTTAAACAGACTTGTATGGGAAACCTTTTGATGA	880
Db	1274	TTTGCCAACTGTTTAATAAGATGGAGAGAATACTGGC--AGGTTTAAGCTTTTCAACCG	1331
Qy	881	TGCAGATCAACAGCATTTTTCGAGGCTTTTGTGATCTTTTTGTGGACTTGGCATCAACAACAC	940
Db	1332	AAATGAGCAACAGTTTCTGGAAGCTTTTGTCACTTTTGTGGCTTGGGGATCCGAACAC	1391
Qy	941	AATTATGATATGATCAAGTGAAGAAGTCTCTGGGCCAACAGCTCTGTGCTCTTGTATGTGCT	1000
Db	1392	GCAGATGATGAAGCAGTGGAGAGAGCCATGGGCCAAGCAATGGTTCACATTTGGAGGTCT	1451
Qy	1001	ATCATAGCATGCAACATGTTTCAAAAGCTGAAGTTGACAAGTTTAAGCGACGCCAACATCCC	1060
Db	1452	GTGCTATCATGCTTCCACACGAGGAAGAAACAAGAGACTACAGTCGTTAGCGGCTGC	1511
Qy	1061	TCGTGGTGTCA-----GAACCTGCCATCGATGACATTCATTTGTGATGACTTTTCTCT	1111
Db	1512	TGTGGTGCCATCTGCCACAGACCCCTTAAATTTACTGACTTTTAGCTTTCAGTGACTTTGAGCT	1571
Qy	1112	CGAGGTTGATGCCATGATCAGCTGCTCTCCCGATGTTTCATGGAGCTGGGGATGGTACA	1171
Db	1572	GTCGTGATCTCGGAACAGCACTGTGTACAATTCGGATGTTTACTGACCTCAACCTGTGCA	1631
Qy	1172	GAATTTTAAAAATTGACTATCAGACACTGTCTAGTGGCTTTTGACAGTGAAGGAACACTA	1231
Db	1632	GAACCTCCAGATGAAACATGAGGTTCTTTCGACATGGATTTTAAGTCTTAAGAAGAAATTA	1691
Qy	1232	TCGGATG---GTTCTTATACCACAACCTGGAGACATGCCCTTCAACGTGTGTCAGCTGATGTT	1288
Db	1692	TCGGAAGAATGTTTGCCTATCATTAATTGGAGACATGCCCTTTAATACAGCTCACTGTCAGT	1751

Db	1411	TTTGCCAACTGTTTAATAGATGGAGGAGATACTGGC--AAGGTTAAGCCTTTCAACGG	1468
QY	881	TGCAGATCAACAGCATTGTTAGGCTTTTGTGCTCATCTTTGTGACATTGGCATCAACAAC	940
Db	1469	AAATGACGAACAGATTCTGGAAGCTTTGTCATCTTTGTGCTTTGGGATCCACAAC	1528
QY	941	AATATGTATGATCAAGTGAAGAAGTCTGGGCCAAGCAGTGTGGGCTCTTTGATGTGCT	1000
Db	1529	GCAGATGTATGAAGCAGTGGAGAGCCTAGGCCAAGCAAAATGGTCACATTTGAGGTTCT	1588
QY	1001	ATCATACCATCAACATGTTCAAAAGCTCAAGTTGACAAAGTTTAAGGCAGCAACATCCC	1060
Db	1589	GTGCTATCATGCTTCAGCAGCAGAGGAAGAAACAAGAGAGCTACAGTCTTAGCGGCTGC	1648
QY	1061	TCGTGCTGTC-----GAACTTGGCCATCGATGACATTCATTTTGTGACTTTTCTCT	1111
Db	1649	TGTGCTGCCATCTGCCAGACCCTTAAATTAATCTAGCTTTCAGTGGCTTTGAGCT	1708
QY	1112	CGACCTTGATGCCATGATCAGCTGCTCTCGGATGTTCAATGGAGCTGGGATGGTACA	1171
Db	1709	GTCTGATCTGGAACAGCAGCTGTGTACAATTCGGATGTTTACTGACCTCAACCTTGTGCA	1768
QY	1172	GAATTTAAATTTGACTATGACACACTGTGTAGTGGCTTTTGACAGTCAGGAAAAACTA	1231
Db	1769	GAACCTCCAGATGAACATGAGGTTCTTTCAGATGGATTTTAAGTGTAAAGAAGAAATTA	1828
QY	1232	TCGGATG---GTTCTATACCAACACTGGAGACATGCTTCAACGTGTGTCAAGCTGATGTT	1288
Db	1829	TCGGAAGATGTTGGCTATCATTAATTTGAGACATGCCCTTAATACAGTCAGTGCATGTT	1888
QY	1289	CCGATGTTAACCATGCTGTGGTCTTCAAGACATTCGACCGAGGTGGAAATTTAGCGGT	1348
Db	1889	TCGTGCTCTAAAAGCAGGCAAAATTCAGAAACAGCTGACTGACCTGGAGATACTTGCATT	1948
QY	1349	GATTTGGGATGCCGTGCTCATGACCTCGACCACAGGGGAACCAACATGCCCTTCCAAGC	1408
Db	1949	GCTGATGCTGCATGAAGCCACGATTTGGATCACCCTGGTGTGAATAACTCTTACATACA	2008
QY	1409	TAAAGTGGCTCTGCCCTGGCCCAACTCTATGGAACCTCTGCTAGCTTGGAGCATCACCA	1468
Db	2009	CGGAAGTGAACATCCACTTGCCCGAGCTTTACTG---CCATTCAATCATGGAACACATCA	2065
QY	1469	TTTCAACACGCGGTGATGATCCCTTCAAGTGAGGGTCACAATATCTTTGCTAACTGTC	1528
Db	2065	TTTTCACCAAGTGCCTGATGATTTCTTAATAGTCCAGCAATCAGATTCAGTGGCTCTC	2125
QY	1529	CTCCAAGGAATATAGTACCTTTATCGACCTTTTGAAGCAGTCAATATTGGCAACAGACCT	1588
Db	2126	CATTGAAGAATATAAGACCACGTTGAAAATAATCAAGCAAGCTATTTTAGCTACAGACCT	2185
QY	1589	CACGCTGTACTTTGAGAGAGAACTGAATTTCTTGAACCTTGTCAAGTAAAGGAGATACGA	1648
Db	2186	AGCACTGTACATTAGAGCGGAGGAGAAATTTTGAACCTTATAAGAAAAATCAATCAA	2245
QY	1649	TTGGAACATCAAAAACCATCGTGATATATTTCCGATCAATGTTTAATGACAGCCTGTACCT	1708
Db	2246	TTTGGAAAGATCTCATCAAAAGGAGTGTGTTTGGCAATGCTGATCAGACGCTTGTGATCT	2305
QY	1709	TGGAGCCGTGACCAACCCGTGGGAGATCTCCAGACAGGTGGGAGAACTTGTAAACAGTGA	1768
Db	2306	TTCTGCAATTTACAAAACCCCTGGCCCTATTCAACACGGATAGCAGAACTTTGTAGCAACTGA	2365
QY	1769	GTTCTTCGAACAGGAGATCGGAGAGATTAGAGCTCAAACTCACTCCCTTCAGCAATTTT	1828
Db	2366	ATTTTTTGTATCAAGGAGCAGAGAGAGAAAGAACTCAACATAGAACCCACTGATCTAAT	2425
QY	1829	TGATCGGAACCGGAAGGATGAATCCCTCGGTTCGAACCTGGAGTGGATTTGATAGCATCTG	1888
Db	2426	GAACAGGGAGAGAAAAACAAAATCCCAAGTATGCAAGTTGGGTTTCATAGATGCCATCTG	2485
QY	1889	CATGCCCTTTGTATCAGGCACTGGTGAAGTCAACGTGAACCTGAAGCCCATGCTAGATTC	1948
Db	2486	CTTGCAACTGTATGAGGCCCTGACCCACGTCAGAGGACTGTTTCCCTTTTCTAGATGG	2545

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Job time : 5428 secs

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